

FIG.1A.

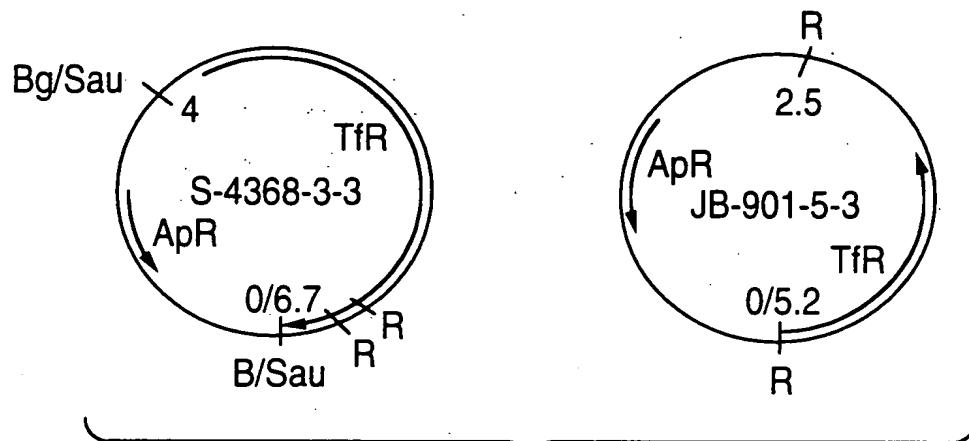


FIG.1B.

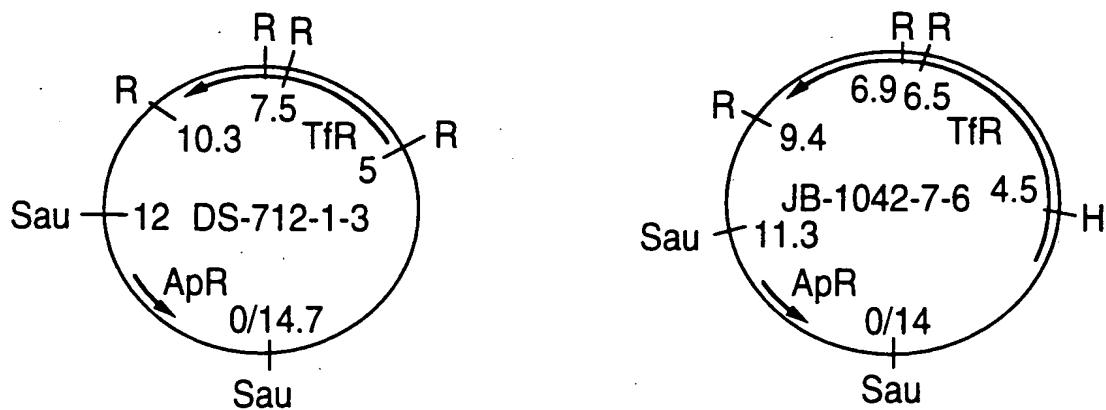


FIG.1C.

FIG.1D.

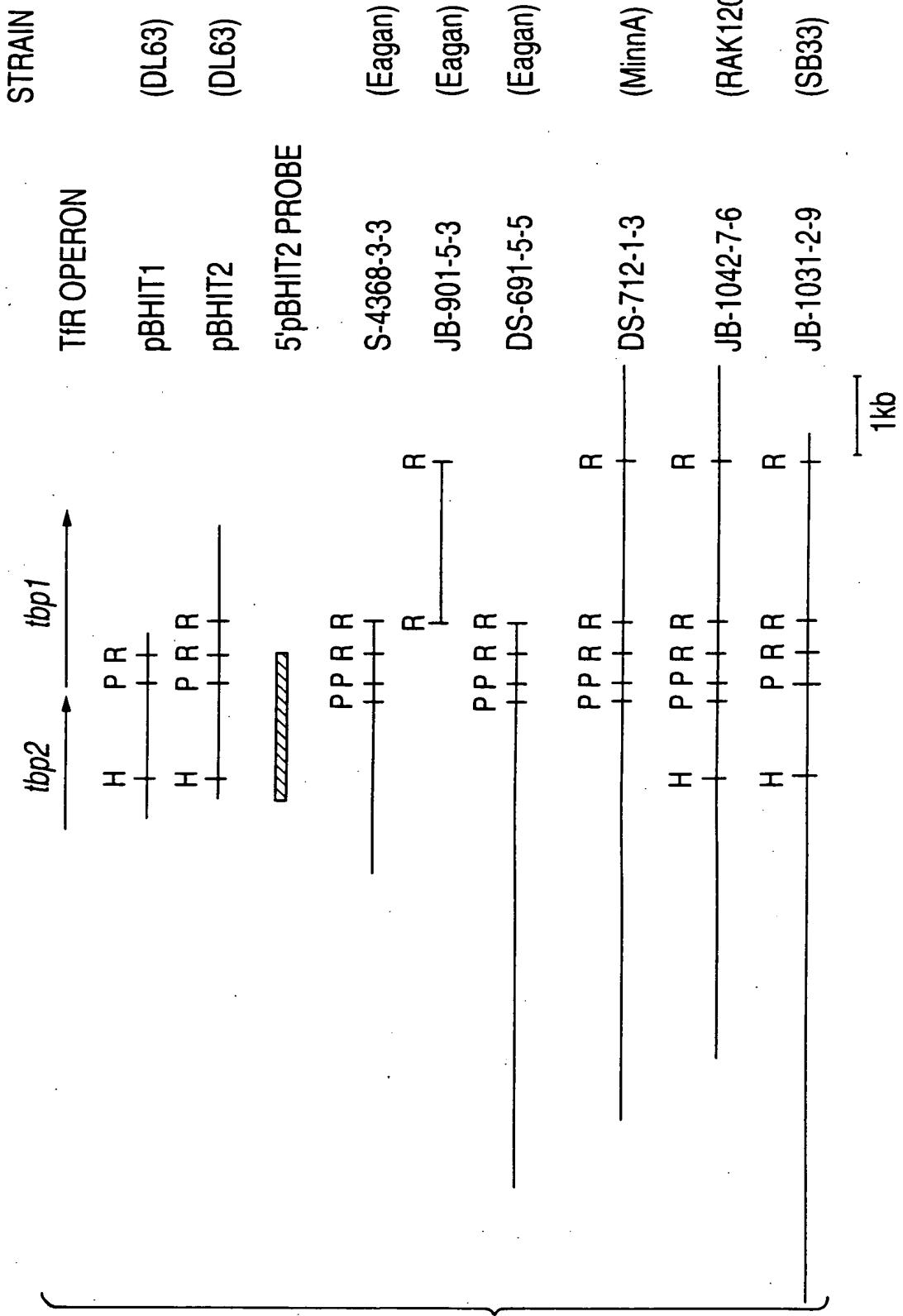


FIG. 2.

FIG. 3 A.

TATAACTA ATG AAA TCT GTC CCT ATC TCT GGT GGA CTT TCC TTT
Met Lys Ser Val Pro Leu Ile Ser Gly Gly Leu Ser Phe
1 5 10

TTC CTA ACT GCT TGT AGC GGA GCG GCG TCT TTT GAT GTC GAT AAC GTC
Leu Leu Ser Ala Cys Ser Gly Gly Ser Phe Asp Val Asp Asn Val
15 20 25

TCT AAT ACC CCC TCT TCT AAA CCA CGT TAT CAA GAC GAT ACT TCA AGT
Ser Asn Thr Pro Ser Ser Lys Pro Arg Tyr Gln Asp Asp Thr Ser Ser
30 35 40 45

TCA AGA ACA AAA TCT AAA TTG GAA AAG TTG TCC ATT CCT TCT TTA CGG
Ser Arg Thr Lys Ser Lys Leu Glu Lys Leu Ser Ile Pro Ser Leu Gly
50 55 60

CGA GGG ATG AAG TTA CGG CCT CTG AAT CTT TTT GAT AGG AAC AAA CCT
Gly Gly Met Lys Leu Ala Ala Leu Asn Leu Phe Asp Arg Asn Lys Pro
65 70 75

AGT CTC TTA AAT GAA GAT AGC TAT ATG ATA TTT TCC TCA CGT TCT ACG
Ser Leu Leu Asn Glu Asp Ser Tyr Met Ile Phe Ser Ser Arg Ser Thr
80 85 90

FIG. 3 B.

ATT GAA GAG GAT GTT AAA AAT GAC AAT CAA AAC GCA GGC GAG CAC CCT ATT
Ile Glu Glu Asp Val Lys Asp Asn Gln Asn Gly Glu His Pro Ile
95 100 105

GAC TCA ATA GTC GAT CCT AGA GCA CCA AAT TCA AAC GAA AAT CGT CAT
Asp Ser Ile Val Asp Pro Arg Ala Pro Asn Ser Asn Glu Asn Arg His
110 115 120 125

CGA CAA AAA TAT GTA TAT TCA GGG CTT TAT ATT CAA TCG TCG AGT
Gly Gln Lys Tyr Val Tyr Ser Gly Leu Tyr Tyr Ile Gln Ser Trp Ser
130 135 140 145

CTA AGA GAT TTA CCA AAT AAA AAG TTT TAT TCA GGT TAC TAT GGA TAT
Leu Arg Asp Leu Pro Asn Lys Lys Phe Tyr Ser Gly Tyr Tyr Gly Tyr
145 150 155 160

GGG TAT TAC TTT GGC AAT ACA ACT GCC TCT GCA TTA CCT GTA GGT GGC
Ala Tyr Tyr Phe Gly Asn Thr Thr Ala Ser Ala Leu Pro Val Gly Gly
165 170 175 180

GTA GCA ACG TAT AAA GCA ACT TGG AGC TTC ATC ACC GCA GCT GAA AAT
Val Ala Thr Tyr Lys Gly Thr Trp Ser Phe Ile Thr Ala Ala Glu Asn
175 180 185

FIG. 3C.

GGC AAG AAT TAT GAA TTT TTA AGA AAT TCT CGT GGC CGT CAA CCT TAT
Gly Lys Asn Tyr Glu Leu Arg Asn Ser Gly Gly Gln Ala Tyr
195 200 205

TCT CGA CGT AGT CCT ACT CCA GAA GAT ATT GAT TTA GAT CGT AAG ACG
Ser Arg Arg Ser Ala Thr Pro Glu Asp Ile Asp Leu Asp Arg Lys Thr
210 215 220

GGC TTA ACA AGT GAA TTT ACT GTC AAT TTT GGT ACA AAA AAG CTC ACT
Gly Leu Thr Ser Glu Phe Thr Val Asn Phe Gly Thr Lys Lys Leu Thr
225 230 235

CGA GGA CTT TAT TAT AAT TTA CGT GAA ACA GAT CCT AAT AAA TCA CAA
Gly Gly Leu Tyr Tyr Asn Leu Arg Glu Thr Asp Ala Asn Lys Ser Gln
245 250

AAT AGA ACA CAT AAA CTC TAC GAT CTA GAA GCT GAT GTT CAT AGC AAC
Asn Arg Thr His Lys Leu Tyr Asp Leu Glu Ala Asp Val His Ser Asn
255 260 265

CGA TTC ACG CGT AAA GTA AAG CCA ACC AAA AAA GAG TCT TCT GAA GAA
Arg Phe Arg Gly Lys Val Lys Pro Thr Lys Glu Ser Ser Glu Glu
270 275 285

F | G. 3 D.

CAT CCC TTT ACC ACC GAG GGA ACA TTA GAA GGT GGT TTT TAC CGG CCT
His Pro Phe Thr Ser Glu Gly Thr Leu Glu Gly Gly Phe Tyr Gly Pro
290 295 300

GAG CGT CAA GAA TTA CGA CGA AAG TTT TTA GCT CAC GAC AAA AAA GTT
Glu Gly Gln Glu Leu Gly Lys Phe Leu Ala His Asp Lys Lys Val
305 310 315

TTC GGG GTA TTT AGT GCC AAA GAA CAG CAA GAA ACG TCA GAA AAC AAC AAA
Leu Gly Val Phe Ser Ala Lys Glu Gln Gln Glu Thr Ser Glu Asn Lys
320 325 330

AAA TTA CCC AAA GAA ACC TTA ATT GAT GGC AAG CTA ACT ACT TTT AAA
Lys Leu Pro Lys Glu Thr Leu Ile Asp Gly Lys Leu Thr Thr Phe Lys
335 340 345

ACA ACC AAT GCA ACA GCC AAT GCA ACA ACC GAT GCA ACA ACC AGT ACA
Thr Thr Asn Ala Thr Ala Asn Ala Thr Thr Asp Ala Thr Thr Ser Thr
350 355 360 365

ACA GCC AGT ACA AAA ACC GAT ACA ACA ACC AAT GCA ACA GCC AAT ACA
Thr Ala Ser Thr Lys Thr Asp Thr Thr Asn Ala Thr Ala Asn Thr
370 375 380

FIG. 3E.

GAA AAC TTT ACC ACA AAA GAT ATA CCA AGT TTT GGT GAA GCT GAT TAT
Glu Asn Phe Thr Thr Lys Asp Ile Pro Ser Leu Gly Glu Ala Asp Tyr
385 390 395

CTT TTA ATT GAT AAT TAC CCT GTT CCT CTT TTC CCT GAG AGT GGT GAT
Leu Leu Ile Asp Asn Tyr Pro Val Pro Leu Phe Pro Glu Ser Gly Asp
400 405 410

TTC ATA AGT AGT AAG CAC CAT ACT GTA GGA AAG AAA ACC TAT CAA GTA
Phe Ile Ser Ser Lys His Thr Val Gly Lys Lys Thr Tyr Gln Val
415 420 425

GAA GCA TGT TGC AGT AAT CTA AGC TAT GTA AAA TTT GGT ATG TAT TAT
Glu Ala Cys Cys Ser Asn Leu Ser Tyr Val Lys Phe Gly Met Tyr Tyr
430 435 440 445

GAA GCC CCA CCT AAA GAA GAA AAA GAA AAA GAC AAA GAC
Glu Ala Pro Pro Lys Glu Glu Lys Glu Lys Asp Lys Asp
450 455 460

AAA GAA AAA GAA CAA GCG ACA ACA TCT ATC AAG ACT TAT TAT CAA
Lys Glu Lys Glu Lys Glu Lys Glu Lys Ser Ile Lys Thr Tyr Tyr Gln
465 470 475

FIG. 3F.

TTC TTA TTA GGT CTC CGT ACT CCC AGT TCT GAA ATA CCT AAA GAA GGA
Phe Leu Leu Gly Leu Arg Thr Pro Ser Ser Glu Ile Pro Lys Glu Gly
480 485 490 495

AGT GCA AAA TAT CAT GGT AAT TCG TTT GGT TAT ATT AGT GAT GGC GAG
Ser Ala Lys Tyr His Gly Asn Tri Phe Gly Tyr Ile Ser Asp Gly Glu
500 505

ACA TCT TAC TCC GCC AGT GGT GAT AAG GAA CGC AGT AAA AAT GCT GTC
Thr Ser Tyr Ser Ala Ser Gly Asp Lys Glu Arg Ser Lys Asn Ala Val
510 515 520 525

GCC GAG TTT AAT GTA AAT TTT GCC GAG AAA ACA TTA ACA GGC GAA TTA
Ala Glu Phe Asn Val Asn Phe Ala Glu Lys Thr Leu Thr Gly Glu Leu
530 535 540

AAA CGA CAC GAT ACT CAA AAT CCC GTA TTT AAA ATT AAT GCA ACC TTT
Lys Arg His Asp Thr Gln Asn Pro Val Phe Lys Ile Asn Ala Thr Phe
545 550 555

CAA AGT GGT AAG AAT GAC TTC ACT GGT ACA GCA ACC GCA AAA GAT TTA
Gln Ser Gly Lys Asn Asp Phe Thr Gly Thr Ala Thr Ala Lys Asp Leu
560 565 570

FIG. 3 G.

GCA ATA GAT CGT AAA AAT ACA CAA CGC ACA TCT AAA GTC AAT TTC ACG
Ala Ile Asp GLY Lys Asn Thr Gln GLY Thr Ser Lys Val Asn Phe Thr
575 580 585

GCA ACA GTA AAC CGG GCA TTT TAT GGT CCG CAC GCT ACA GAA TTA GCC
Ala Thr Val Asn GLY Ala Phe Tyr GLY Pro His Ala Thr GLU Leu GLY
590 595 600 605

GGT TAT TTC ACC TAT AAC GGA AAC AAT CCT ACA GAT AAA AAT TCA TCA
Gly Tyr Phe Thr Tyr Asn Gly Asn Asn Pro Thr Asp Lys Asn Ser Ser
610 615 620

TCC AAT TCA GAA AAG GCA AGA GCT GCC GTT GTG TTT GGA GCT AAA AAA
Ser Asn Ser Glu Lys Ala Arg Ala Val Val Phe Gly Ala Lys Lys
625 630 635

CAA CAA GTA GAA ACA ACC AA GAA GTAAATGGAAT ACTAAAA A ATG ACT AAA AAA
Gln Gln Val Glu Thr Thr Lys
640 645

CCC TAT TTT CGC CTA AGT ATT ATT TCT TGT CTT TTA ATT TCA TGC TAT
Pro Tyr Phe Arg Leu Ser Ile Ile Ser Cys Leu Leu Ile Ser Cys Tyr
650 655 660

FIG. 3H.

GTA AAA GCA GAA ACT CAA AGT ATA AAA GAT ACA AAA GAA GCT ATA TCA
Val Lys Ala Glu Thr Gln Ser Ile Lys Asp Thr Lys Glu Ala Ile Ser
665 670 675 680

TCT GAA GTG GAC ACT CAA AGT ACA GAA GAT TCA GAA TAA GAA ACT ATC
Ser Glu Val Asp Thr Gln Ser Thr Glu Asp Ser Glu Leu Glu Thr Ile
685 690 695

TCA GTC ACT GCA GAA AAA GTT AGA GAT CGT AAA GAT AAT GAA GTA ACT
Ser Val Thr Ala Glu Lys Val Arg Asp Arg Lys Asp Asn Glu Val Thr
700 705 710

GGA CTT GGC AAA ATT ATA AAA ACT AGT GAA AGT ATC AGC CCA GAA CAA
Gly Leu Gly Lys Ile Ile Lys Thr Ser Glu Ser Ile Ser Arg Glu Gln
715 720 725

GTA TTA ATT ATT CGT GAT CTA ACA CGC TAT GAT CCA GGG ATT TCA GTT
Val Leu Asn Ile Arg Asp Leu Thr Arg Tyr Asp Pro Gly Ile Ser Val
730 735 740

GTA GAA CAA GGT CGC GGT GCA AGT TCT GGA TAT TCT ATT CGT GGT ATG
Val Glu Gln Gly Arg Gly Ala Ser Ser Gly Tyr Ser Ile Arg Gly Met
745 750 755 760

FIG. 31.

GAAC AGA AAT AGA GTT GCT TTA TTA GAT GGT TTA CCT CAA ACG CAA
Asp Arg Asn Arg Val Ala Leu Leu Val Asp Gly Leu Pro Gln Thr Gln
765 770 775

TCT TAT GTA GTG CAA AGC CCT TTA GTT GCT CGT TCA GGA TAT TCT GGC
Ser Tyr Val Val Gln Ser Pro Leu Val Ala Arg Ser Gly Tyr Ser Gly
780 785 790 795

ACT GGT GCA ATT AAT GAA ATT GAA TAT GAA AAT GTC AAG CCC GTC GAA
Thr Gly Ala Ile Asn Glu Ile Glu Tyr Glu Asn Val Lys Ala Val Glu
795 800 805

ATA AGC AAG CGG CGG AGT TCT GAG TAT GGT ATT GGA GCA CTA GCT
Ile Ser Lys Gly Ser Ser Ser Glu Tyr Gly Asn Gly Ala Leu Ala
810 815 820 825

GGT TCT GTA ACA TTT CAA AGC AAA TCA GCA GCC GAT ATC TTA GAA GGA
Gly Ser Val Thr Phe Gln Ser Lys Ser Ala Ala Asp Ile Leu Glu Gly
830 835 840 845

GAC AAA TCA TCG CGA ATT CAA ACT AAA AAT GCT TAT TCA AGC AAA AAT
Asp Lys Ser Thr Gly Ile Glu Thr Lys Asn Ala Tyr Ser Ser Lys Asn
850 855

FIG. 3 J.

AAA GGC TTT ACC CAT TCT TTA GCT GTA GCA GGA AAA CAA CGG GGA TTT
Lys Gly Phe Thr His Ser Leu Ala Val Ala Gly Lys Gln Gly Gly Phe
860 865 870

GAA GGG GTC GCC ATT TAC ACT CAC CGA AAT TCA ATT GAA ACC CAA GTC
Glu Gly Val Ala Ile Tyr Thr His Arg Asn Ser Ile Glu Thr Gln Val
875 880 885

CAT AAA GAT GCA TTA AAA GGC GTG CAA AGT TAT GAT CGA TTC ATC GCC
His Lys Asp Ala Leu Lys Gly Val Gln Ser Tyr Asp Arg Phe Ile Ala
890 895 900

ACA ACA GAG GAT CAA TCT GCA TAC TTT GTG ATG CAA GAT GAG TGT CTA
Thr Thr Glu Asp Gln Ser Ala Tyr Phe Val Met Gln Asp Glu Cys Leu
905 910 915

GAT GGT TAT GAC AAG TGT AAA ACT TCA CCC AAA CGA CCT GCG ACT TTA
Asp Gly Tyr Asp Lys Cys Lys Thr Ser Pro Lys Arg Pro Ala Thr Leu
925 930 935

TCC ACC CAA AGA GAA ACC GTA AGC GTT TCA GAT TAT ACG GGG GCT AAC
Ser Thr Gln Arg Glu Thr Val Ser Val Ser Asp Tyr Thr Gly Ala Asn
940 945 950

F16.3K.

CGT ATC AAA CCT AAT CCA ATG AAA TAT GAA AGC CAG TCT TGG TTT TTA
Arg Ile Lys Pro Asn Pro Met Lys Tyr Glu Ser Gln Ser Trp Phe Leu
955 960 965

AGA GGA GGT TAT CAT TTT TCT GAA CAA CAC TAT ATT GGT GGT ATT TTT
Arg Gly Gly Tyr His Phe Ser Glu Gln His Tyr Ile Gly Gly Ile Phe
970 975 980

GAA TTC ACA CAA CAA AAA TTT GAT ATC CGT GAT ATG ACA TTT CCC GCT
Glu Phe Thr Gln Gln Lys Phe Asp Ile Arg Asp Met Thr Phe Pro Ala
985 990 995

TAT TTA AGG CCA ACA GAA GAC AAG GAT TTA CAA AGT CGC CCT TTT TAT
Tyr Leu Arg Pro Thr Glu Asp Lys Asp Leu Gln Ser Arg Pro Phe Tyr
1000 1010 1015

CCA AAG CAA GAT TAT GGT GCA TAT CAA CAT ATT GGT GAT GGC AGA GGC
Pro Lys Gln Asp Tyr Gly Ala Tyr Gln His Ile Gly Asp Gly Arg Gly
1020 1025 1030

GTT AAA TAT GCA AGT GGG CTT TAT TTC GAT GAA CAC CAT AGA AAA CAG
Val Lys Tyr Ala Ser Gly Leu Tyr Phe Asp Glu His His Arg Lys Gln
1035 1040 1045

FIG. 3 L.

CGT GTA CGT ATT GAA TAT ATT TAC GAA AAT AAG AAC AAA GCG GGC ATC
Arg Val Gly Ile Glu Tyr Ile Tyr Glu Asn Lys Ala Gly Ile
1055 1060

ATT GAC AAA GCG GTG TTA AGT GCT AAT CAA CAA ACA TCA TAC TTG ACA
Ile Asp Lys Ala Val Leu Ser Ala Asn Gln Gln Thr Ser Tyr Leu Thr
1065 1070 1075 1080

GTT ATA TGC GAC ATA CGC ATT GCA GTC TTT ATC CAT AAT CCA AGT AAG
Val Ile Cys Asp Ile Arg Ile Ala Val Phe Ile His Asn Pro Ser Lys
1085 1090 1095

AAT TGC CGC CCA ACA CTT GAT AAA CCT TAT TCA TAC TAT CAT TCT GAT
Asn Cys Arg Pro Thr Leu Asp Lys Pro Tyr Ser Tyr His Ser Asp
1100 1105 1110

AGA AAT GTT TAT AAA GAA AAA CAT AAC ATG TTG CAA TTG ATT TTA GAG
Arg Asn Val Tyr Lys Glu Lys His Asn Met Leu Gln Leu Asn Leu Glu
1115 1120 1125

AAA AAA ATT CAA CAA AAT TCG CTT ACT CAT CAA ATT GCC TTC AAT CTT
Lys Lys Ile Gln Gln Asn Trp Leu Thr His Gln Ile Ala Phe Asn Leu
1130 1135 1140

FIG. 3 M.

CGT TTT GAT GAC TTT ACT TCC GCA CTT CAG CAT AAA GAT TAT TTA ACT
Gly Phe Asp Asp Phe Thr Ser Ala Leu Gln His Lys Asp Tyr Leu Thr
1145 1150 1155 1160

CGA CGT GTT ATC GCT ACG GCA AGT AGT ATT TCA GAG AAA CGT GGT GAA
Arg Arg Val Ile Ala Thr Ala Ser Ser Ile Ser Glu Lys Arg Gly Glu
1165 1170 1175

GCA AGA AGA AAT CGT TTA CAA TCA AGT CCT TAC TTA TAC CCA ACA CCA
Ala Arg Arg Asn Gly Leu Gln Ser Ser Pro Tyr Leu Tyr Pro Thr Pro
1180 1185 1190 1195

AAA GCA GAG TTG GTA CGA CGA GAT CTT TGT AAT TAT CAA CGT AAG TCC
Lys Ala Glu Leu Val Gly Gly Asp Leu Cys Asn Tyr Gln Gly Lys Ser
1195 1200 1205

TCT AAT TAC AGT GAC TGT AAA GTG CGG TTA ATT AAA GGG AAA AAT TAT
Ser Asn Tyr Ser Asp Cys Lys Val Arg Leu Ile Lys Gly Lys Asn Tyr
1210 1215 1220

TAT TTC CCA CGA CGC AAT AAT ATG GCA TTA CGG AAA TAC GTT GAT TTA
Tyr Phe Ala Ala Arg Asn Asn Met Ala Leu Gly Lys Tyr Val Asp Leu
1225 1230 1235 1240

FIG. 3 N.

GGT TTA GGT ATG AGG TAT GAC GTC TCT CGT ACA AAA GCT AAT GAA TCA
Gly Leu Gly Met Arg Tyr Asp Val Ser Arg Thr Lys Ala Asn Glu Ser
1245 1250

ACT ATT AGT GTT CGT AAA TTT AAA ATG TTC TCT TCG AAT ACT GGT ATT
Thr Ile Ser Val Gly Lys Phe Lys Asn Phe Ser Thr Asn Thr Gly Ile
1260 1265 1270

GTC ATA AAA CCA ACG GAA TGG CTT GAT CTT TCT TAT CGC CCT TCT ACT
Val Ile Lys Pro Thr Glu Trp Leu Asp Leu Ser Tyr Arg Leu Ser Thr
1275 1280 1285

GGA TTT AGA AAT CCT AGT TTT GCT GAA ATG TAT CGT TGG CGG TAT CGT
Gly Phe Arg Asn Pro Ser Phe Ala Glu Met Tyr Gly Trp Arg Tyr Gly
1290 1295 1300

GGC AAG GAT ACC GAT GTT TAT ATA GGT AAA TTT AGG CCT GAA ACA TCT
Gly Lys Asp Thr Asp Val Tyr Ile Gly Lys Phe Lys Pro Glu Thr Ser
1305 1310 1315

CGT AAC CAA GAG TTT CGT CTC GCT CTA AAA GGG GAT TTT CGT AAT ATT
Arg Asn Gln Glu Phe Gly Leu Ala Leu Lys Gly Asp Phe Gly Asn Ile
1325 1330 1335

FIG. 30.

GAG ATC AGT CAT TTT AGT AAT GCT TAT CGA AAT CTT ATC GGC TTT GCT
Glu Ile Ser His Phe Ser Asn Ala Tyr Arg Asn Leu Ile Ala Phe Ala
1340 1345 1350

GAA GAA CTT AGT AAA AAT GGA ACT ACT GGA AAG GGC AAT TAT GGA TAT
Glu Glu Leu Ser Lys Asn Gly Thr Thr Gly Lys Gly Asn Tyr Gly Tyr
1355 1360 1365

CAT AAT GCA CAA AAT GCA AAA TTA GTT GCG GTC AAT ATA ACT GCG CAA
His Asn Ala Gln Asn Ala Lys Leu Val Gly Val Asn Ile Thr Ala Gln
1370 1375 1380

TTA GAT TTT AAT GGT TTA TCG AAA CGT ATT CCC TAC GGT TGG TAT GCA
Leu Asp Phe Asn Gly Leu Trp Lys Arg Ile Pro Tyr Gly Trp Tyr Ala
1385 1390 1395

ACA TTT GCT TAT AAC CGA GTA AAA GTT AAA GAT CAA AAA ATC AAT GCT
Thr Phe Ala Tyr Asn Arg Val Lys Val Lys Asp Gln Lys Ile Asn Ala
1405 1410 1415

CGT TTA GCT TCC GTA AGC AGT TAT TTA TTT GAT GCC ATT CAG CCC AGC
Gly Leu Ala Ser Val Ser Ser Tyr Leu Phe Asp Ala Ile Gln Pro Ser
1420 1425 1430

F16.3 P.

CGT TAT ATC ATT GGT TTA GGC TAT GAT CAT CCA AGT AAT ACT TGG CGA
Arg Tyr Ile Ile Gly Leu Gly Tyr Asp His Pro Ser Asn Thr Trp Gly
1435 1440 1445

ATT AAG ACA ATG TTT ACT CAA TCA AAA GCA AAA TCT CAA AAT GAA TTTG
Ile Lys Thr Met Phe Thr Gln Ser Lys Ala Lys Ser Gln Asn Glu Leu
1450 1455 1460

CTA GGA AAA CGT GCA TTG GGT AAC AAT TCA AGG AAT GTA AAA TCA ACA
Leu Gly Lys Arg Ala Leu Gly Asn Asn Ser Arg Asn Val Lys Ser Thr
1465 1470 1475

AGA AAA CTT ACT CGG GCA TGG CAT ATC TTA GAT GTA TCG GGT TAT TAC
Arg Lys Leu Thr Arg Ala Thr His Ile Leu Asp Val Ser Gly Tyr Tyr
1485 1490 1495

ATG GTG AAT AGA AGT ATT TTG TTC CGA TTA GGA GAA TAT AAT TTA TTA
Met Val Asn Arg Ser Ile Leu Phe Arg Leu Gly Val Tyr Asn Leu Leu
1500 1505 1510

AAC TAT CGC TAT GTC ACT TGG GAA GCG GTG CGT CAA ACA GCA CAA CGT
Asn Tyr Arg Tyr Val Thr Trp Glu Ala Val Arg Gln Thr Ala Gln Gly
1515 1520 1525

F 16.3 Q.

GCG GTC AAT CAA CAT CAA AAT GTT GGT AAC TAT ACT CGC TAC GCA GCA
Ala Val Asn Gln His Gln Asn Val Gly Asn Tyr Thr Arg Tyr Ala Ala
1530 1535 1540

TCA CGA CGA AAC TAT ACC TTA ACA TTA GAA ATG AAA TTC TAA
Ser Gly Arg Asn Tyr Thr Leu Thr Leu Glu Met Lys Phe
1545 1550 1555

FIG. 4 A.

CCCCAAGCTA CATCGTTAA TGATAAGCT ATAAATCGATA AGAAAGAAAT TGTGTTTACG

CCATTCTTCA TATTTTATCC ATGAACTTAA AAAACTCTAA ⁻³⁵CTTGACATTA TTACAAAAA

⁻¹⁰AGATCAATTAA TCCGAATTAT TATCATTTT ⁻⁸⁵GTATGAGTAT ATAAATCT ATG AAA TCT

Met Lys Ser
1

GTA CCT ATC TCT GGT GGA CTT TCC TTT TTA CTA AGT GCT TGT AGC
Val Pro Leu Ile Ser Gly Leu Ser Phe Leu Ser Ala Cys Ser
5 10 15

GGA GGG GGG TCT TTT GAT GTA GAT AAC GTC TCT AAT ACC CCC TCT TCT
Gly Gly Ser Phe Asp Val Asp Asn Val Ser Asn Thr Pro Ser Ser
20 25 30 35

AAA CCA CGT TAT CAA GAC GAT ACC TCG AAT CAA AGA AAA AAA TCT ATT
Lys Pro Arg Tyr Gln Asp Thr Ser Asn Gln Arg Lys Lys Ser Asn
40 45 50

TTG AAA AAG TTG TTC ATT CCT CCT TTA GGA GGA GGG ATG AAA TTG GTG
Leu Lys Leu Phe Ile Pro Ser Leu Gly Gly Gly Met Lys Leu Val
55 60 65

FIG. 4B.

GCT CAG AAT CTT CGT GGT AAT AAA GAA CCT AGT TTC TTA AAT GAA GAT
Ala Gln Asn Leu Arg Gly Asn Lys Glu Pro Ser Phe Leu Asn Glu Asp
70 75 80

GAC TAT ATA TCA TAT TTT TCC TCA CTT TCT ACG ATT GAA AAG GAT GTT
Asp Tyr Ile Ser Tyr Phe Ser Ser Leu Ser Thr Ile Glu Lys Asp Val
85 90 95

AAA GAT AAC AAA AAC GGG GCG GAC CTT ATT GGC TCA ATA GAC GAG
Lys Asp Asn Asn Lys Asn Gly Ala Asp Leu Ile Gly Ser Ile Asp Glu
100 105 110 115

CCT AGT ACA ACA AAT CCA CCC GAA AAG CAT CAT CGA CAA AAA TAT GTA
Pro Ser Thr Thr Asn Pro Pro Glu Lys His His Gly Gln Lys Tyr Val
120 125 130

TAT TCA CGG CTT TAT TAT ACT CCA TCG TGG AGT TTA AAC GAT TCT AAA
Tyr Ser Gly Leu Tyr Tyr Thr Pro Ser Trip Ser Leu Asn Asp Ser Lys
135 140 145

AAC AAG TTT TAT TTA CGT TAC TAT GGA TAT GCG TTT TAT TAT GGT AAT
Asn Lys Phe Tyr Leu Gly Tyr Tyr Gly Tyr Ala Phe Tyr Tyr Gly Asn
150 155 160

FIG. 4 C.

AAA ACT GCA ACA AAC TTG CCA AAC GGT GTA CCT AAA TAC AAA GGA
Lys Thr Ala Thr Asn Leu Pro Val Asn Gly Val Ala Lys Tyr Lys Gly
165 175

ACT TGG GAT TTC ATC ACT GCA ACT AAA AAT GGC AAA CGT TAT CCT TTG
Thr Trp Asp Phe Ile Thr Ala Thr Lys Asn Gly Lys Arg Tyr Pro Leu
180 185 190 195

TTA AGT AAT CGC AGT CAC GCT TAT TAT CGA CGT AGT GCA ATT CCA GAA
Leu Ser Asn Gly Ser His Ala Tyr Tyr Arg Arg Ser Ala Ile Pro Glu
200 205 210

GAT ATT GAT TTA GAA AAT GAT TCA AAG AAT CGT GAT ATA GGC TTA ATA
Asp Ile Asp Leu Glu Asn Asp Ser Lys Asn Gly Asp Ile Gly Leu Ile
215 220 225

AGT GAA TTT AGT GCA GAT TTT GGG ACT AAA AAA CTG ACA CGA CAA CTG
Ser Glu Phe Ser Ala Asp Phe Gly Thr Lys Lys Leu Thr Gly Gln Leu
230 235 240

TCT TAC ACC AAA AGA AAA ACT AAT AAT CAA CCA TAT GAA AAG AAA AAA
Ser Tyr Thr Lys Arg Lys Thr Asn Asn Gln Pro Tyr Glu Lys Lys Lys
245 250 255

FIG. 4D.

CTC TAT GAT ATA GAT GCC GAT ATT TAT AGT AAT AGA TTC AGG GGT ACA
Leu Tyr Asp Ile Asp Ala Asp Ile Tyr Ser Asn Arg Phe Arg Gly Thr
260 270 275

GTA AAG CCA ACC GAA AAA GAT TCT GAA GAA CAT CCC TTT ACC AGC GAG
Val Lys Pro Thr Glu Lys Asp Ser Glu Glu His Pro Phe Thr Ser Glu
280 285 290

GGA ACA TTA GAA CGT CGT TTT TAT GGG CCT AAT GCT GAA GAA CTA CGG
Gly Thr Leu Glu Gly Phe Tyr Gly Pro Asn Ala Glu Glu Leu Gly
295 300 305

GGG AAA TTT TTA GCT ACG GAT AAC CGA GTT TTT GGG GTA TTT AGT GCC
Gly Lys Phe Leu Ala Thr Asp Asn Arg Val Phe Gly Val Phe Ser Ala
310 315 320

AAA GAA ACG GAA GAA ACA AAA AAG GAA GCG TTA TCC AAG GAA ACC TTA
Lys Glu Thr Glu Glu Thr Lys Lys Glu Ala Leu Ser Lys Glu Thr Leu
325 330 335

ATT GAT CGC AAG CTA ATT ACT TTC TCT ACT AAA AAA ACC GAT GCA AAA
Ile Asp Gly Lys Leu Ile Thr Phe Ser Thr Lys Lys Thr Asp Ala Lys
340 345 355

FIG. 4E.

ACC AAT GCA ACA ACC AGT ACC GCA GCT AAT ACA ACA ACC GAT ACA ACC
Thr Asn Ala Thr Thr Ser Thr Ala Ala Asn Thr Thr Thr Asp Thr Thr
360 365 370

CCC AAT ACA ATA ACC GAT GAA AAA AAC TTT AAG ACG GAA GAT ATA TCA
Ala Asn Thr Ile Thr Asp Glu Lys Asn Phe Lys Thr Glu Asp Ile Ser
375 380 385

AGT TTT GGT GAA GCT GAT TAT CTG TTA ATT GAC AAA TAT CCT ATT CCA
Ser Phe Gly Glu Ala Asp Tyr Leu Ile Asp Lys Tyr Pro Ile Pro
390 395 400

CTT TTA CCT GAT AAA AAT ACT AAT GAT TTC ATA AGT AAG CAT CAT
Leu Leu Pro Asp Lys Asn Thr Asn Asp Phe Ile Ser Ser Lys His His
405 410 415

ACT GTA GCA AAT AAA CGC TAT AAA GTG GAA GCA TGT TGC AGT AAT CTA
Thr Val Gly Asn Lys Arg Tyr Lys Val Glu Ala Cys Ser Asn Leu
420 425 430 435

AGC TAT GTG AAA TTT CGT ATG TAT TAT GAA GAC CCA CTT AAA GAA AAA
Ser Tyr Val Lys Phe Gly Met Tyr Tyr Glu Asp Pro Leu Lys Glu Lys
440 445 450

FIG. 4F.

GAA ACA GAA ACA GAA ACA GAA AAA GAC AAA GAA GAA AAA
Glu Thr Glu Thr Glu Thr Glu Thr Glu Lys Asp Lys Glu Lys
455 460 465

GAA AAA GAC AAA GAC AAA CAA ACG GCG GCA ACG ACC AAC ACT
Glu Lys Asp Lys Glu Lys Gln Thr Ala Ala Thr Thr Asn Thr
470 475 480

TAT TAT CAA TTC TTA TTA CGT CAC CGT ACT CCC AAG GAC GAC ATA CCT
Tyr Tyr Gln Phe Leu Leu Gly His Arg Thr Pro Lys Asp Asp Ile Pro
485 490 495

AAA ACA CGA AGT GCA AAA TAT CAT CGT AGT TGG TTT CGT TAT ATT ACT
Lys Thr Gly Ser Ala Lys Tyr His Gly Ser Trp Phe Gly Tyr Ile Thr
500 505 510

GAC CGT AAG ACA TCT TAC TCC CCC ACT GGT GAT AAG AAA CGC GAT AAA
Asp Gly Lys Thr Ser Tyr Ser Pro Ser Gly Asp Lys Lys Arg Asp Lys
520 525 530

AAT GCT GTC GCC GAG TTT AAT GTT GAT TTT GCC GAG AAA AAG CTA ACA
Asn Ala Val Ala Glu Phe Asn Val Asp Phe Ala Glu Lys Lys Leu Thr
535 540 545

FIG. 4 G.

GCG GAA TTA AAA CGA CAC GAT ACT GGA AAT CCC GTC TTT AGT ATT GAG
Gly Glu Leu Lys Arg His Asp Thr Gly Asn Pro Val Phe Ser Ile Glu
550 555 560

GCA AAC TTT AAT AAT AGT AGT AAT GGC TTC ACT GGT ACA GCA ACC GCA
Ala Asn Phe Asn Asn Ser Ser Asn Ala Phe Thr Gly Thr Ala Thr Ala
565 570 575

ACA AAT TTT GTC ATA GAT GGT AAA AAT AGT CAA AAT AAA AAT ACC CCA
Thr Asn Phe Val Ile Asp Gly Lys Asn Ser Gln Asn Lys Asn Thr Pro
580 585 590

ATT AAT ACA ACT AAA GTC AAC GGG GCA TTT TAT GGA CCT AAG GCT
Ile Asn Ile Thr Thr Lys Val Asn Gly Ala Phe Tyr Gly Pro Lys Ala
600 605 610

TCT GAA TTA GGC GGT TAT TTC ACT TAT AAC GGA AAT TCT ACA GCT ACA
Ser Glu Leu Gly Gly Tyr Phe Thr Tyr Asn Gly Asn Ser Thr Ala Thr
615 620 625

AAT TCT GAA AGT TCC TCA ACC GTC TCT TCA TCA TCC AAT TCA AAA AAT
Asn Ser Glu Ser Ser Ser Thr Val Ser Ser Ser Asn Ser Lys Asn
630 635 640

FIG. 4H.

GCA AGA GCT GCA GTT GTC TTT GGT GCG AGA CAA CAA GTA GAA ACA ACC
Ala Arg Ala Ala Val Val Phe Gly Ala Arg Gln Gln Val Glu Thr Thr
645

AAA TAATGGAATA CTAAAATG ACT AAA AAA CCC TAT TTT CGC CTA AGT
Lys Met Thr Lys Lys Pro Tyr Phe Arg Leu Ser
660 665 670

ATT ATT TCT TGT CTT ATT TCA TGC TAT GTA AAA GCA GAA ACT CAA
Ile Ile Ser Cys Leu Ile Ser Cys Tyr Val Lys Ala Glu Thr Gln
675 680 685

AGT ATA AAA GAT ACA AAA GAA GCT ATA TCA TCT GAA GTG GAC ACT CAA
Ser Ile Lys Asp Thr Lys Glu Ala Ile Ser Ser Glu Val Asp Thr Gln
690 695 700

AGT ACA GAA GAT TCA GAA TTA GAA ACT ATC TCA GTC ACT GCA GAA AAA
Ser Thr Glu Asp Ser Glu Leu Glu Thr Ile Ser Val Thr Ala Glu Lys
705 710 715

ATA AGA GAT CGT AAA GAT AAT GAA GTA ACT GGA CTT GGC AAA ATT ATC
Ile Arg Asp Arg Lys Asn Glu Val Thr Gly Leu Gly Lys Ile Ile
720 725 730

FIG. 41.

AAA ACT AGT GAA AGT ATC AGC CGA GAA CAA GTC TTA AAT ATT CGT GAT
Lys Thr Ser Glu Ser Ile Ser Arg Glu Gln Val Leu Asn Ile Arg Asp
735 740 745 750

CTA ACA CGC TAT GAT CCA CGG ATT TCA GTT GTA GAA CAA CGT CGC CGT
Leu Thr Arg Tyr Asp Pro Gly Ile Ser Val Val Glu Gln Gly Arg Gly
755 760 765

GCA AGT TCT CGA TAT TCT ATT CGT CGT ATG GAC AGA AAT AGA GTT GCT
Ala Ser Ser Gly Tyr Ser Ile Arg Gly Met Asp Arg Asn Arg Val Ala
770 775 780

TTA TTA GTA GAT CGT TTA CCT CAA ACG CAA TCT TAT GTA GTG CAA AGC
Leu Leu Val Asp Gly Ile Pro Gln Thr Gln Ser Tyr Val Val Gln Ser
785 790 795

CCT TTA GTT GCT CGT TCA CGA TAT TCT CGC ACT CGT GCA ATT AAT GAA
Pro Leu Val Ala Arg Ser Gly Tyr Ser Gly Thr Gly Ala Ile Asn Glu
800 805 810

ATT GAA TAT GAA AAT GTC AAG GCG GTC GAA ATA AGC AAG GGG GGG AGT
Ile Glu Tyr Glu Asn Val Lys Ala Val Glu Ile Ser Lys Gly Gly Ser
815 820 825 830

FIG. 4 J.

TCT TCT GAG TAT GGT AAT GGA GCA CTA GCT GGT TCT GTA ACA TTT CAA
Ser Ser Glu Tyr Gly Asn Gly Ala Leu Ala Gly Ser Val Thr Phe Gln
835 840 845

AGC AAA TCA GCA GCC GAT ATC TTA GAA GGA GAC AAA TCA TGG CGA ATT
Ser Lys Ser Ala Ala Asp Ile Leu Glu Gly Asp Lys Ser Trp Gly Ile
850 855 860

CAA ACT AAA AAT GCT TAT TCA AGC AAA AAT AAA GGC TTT ACC CAT TCT
Gln Thr Lys Asn Ala Tyr Ser Ser Lys Asn Lys Gly Phe Thr His Ser
865 870 875

TTA GCT GTA GCA GGA AAA CAA CGT GGA TTT GAA GGG CTA GCC ATT TAC
Leu Ala Val Ala Gly Lys Gln Gly Phe Glu Gly Leu Ala Ile Tyr
880 885 890

ACT CGA AAT TCA ATT GAA ACC CAA GTC CAT AAA GAT GCA TTA AAA
Thr Gln Arg Asn Ser Ile Glu Thr Gln Val His Lys Asp Ala Leu Lys
895 900 905 910

GCG GTA CAA AGT TAT GAT CGA TTA ATC GCC ACA GAT AAA TCT TCA
Gly Val Gln Ser Tyr Asp Arg Leu Ile Ala Thr Thr Asp Lys Ser Ser
915 920 925

FIG. 4K.

CGA TAC TTT GTG ATA CAA GGT GAG TGT CCA AAT GGT GAT GAC AAG TGT
Gly Tyr Phe Val Ile Gln Gly Glu Cys Pro Asn Gly Asp Asp Lys Cys
930 935 940

GCA GCC AAG CCA CCT GCG ACT TTA TCC ACC CAA ACC GAA ACC GTC ACC
Ala Ala Lys Pro Pro Ala Thr Leu Ser Thr Gln Ser Glu Thr Val Ser
945 950 955

GTT TCA GAT TAT ACG GGG GCT AAC CGT ATC AAA CCT AAT CCA ATG AAA
Val Ser Asp Tyr Thr Gly Ala Asn Arg Ile Lys Pro Asn Pro Met Lys
960 965 970

TAT GAA AGC CAG TCT TCG TTT TTA AGA GGA GGG TAT CAT TTT TCT GAA
Tyr Glu Ser Gln Ser Trp Phe Leu Arg Gly Gly Tyr His Phe Ser Glu
975 980 985

CAA CAT TAT ATT GGT GGT ATT TTT GAA TTC ACA CAA AAA TTT GAT
Gln His Tyr Ile Gly Gly Ile Phe Glu Phe Thr Gln Gln Lys Phe Asp
995 1000 1005

ATC CGT GAT ATG ACA TTT CCC GCT TAT TTA AGC CCA ACA GAA AGA CGG
Ile Arg Asp Met Thr Phe Pro Ala Tyr Leu Ser Pro Thr Glu Arg Arg
1010 1015 1020

FIG. 4 L.

GAT GAT AGT AGT CGT TCT TAT CCA ATG CAA GAT CAT GGT GCA TAT
Asp Asp Ser Ser Arg Ser Phe Tyr Pro Met Gln Asp His Gly Ala Tyr
1025 1030 1035

CAA CAT ATT GAG GAT GGC AGA GGC GTT AAA TAT GCA AGT GGG CTT TAT
Gln His Ile Glu Asp Gly Arg Gly Val Lys Tyr Ala Ser Gly Leu Tyr
1040 1045

TTC GAT GAA CAC CAT AGA AAA CAG CGT GTA GGT ATT GAA TAT ATT TAC
Phe Asp Glu His His Arg Lys Gln Arg Val Gly Ile Glu Tyr Ile Tyr
1055 1060 1065

GAA AAT AAG AAC AAA CGG GCG ATC ATT GAC AAA GCA GTG TTA AGT GCT
Glu Asn Lys Asn Lys Ala Gly Ile Ile Asp Lys Ala Val Leu Ser Ala
1075 1080 1085

ATT CAA CAA AAC ATC ATA CTT GAC AGT TAT ATG CGA CAT ACG CAT TGC
Asn Gln Gln Asn Ile Ile Leu Asp Ser Tyr Met Arg His Thr His Cys
1090 1095 1100

AGT CTT TAT CCT AAT CCA AGT AAG AAT TGC CGC CCA ACA CTT GAT AAA
Ser Leu Tyr Pro Asn Pro Ser Lys Asn Cys Arg Pro Thr Leu Asp Lys
1105 1110 1115

FIG. 4 M.

CCT TAT TCA TAC TAT CGT TCT GAT AGA AAT GTT TAT AAA GAA AAA CAT
Pro Tyr Ser Tyr Tyr Arg Ser Asp Arg Asn Val Val Tyr Lys Glu Lys His
1120 1125 1130

AAT ATG TTG CAA TTG AAT TTA GAG AAA AAA ATT CAA CAA AAT TCG CTT
Asn Met Leu Gln Leu Asn Leu Glu Lys Lys Ile Gln Gln Asn Trp Leu
1135 1140 1145 1150

ACT CAT CAA ATT GTC TIC AAT CTT GGT TTT GAT GAC TTT ACT TCA GCG
Thr His Gln Ile Val Phe Asn Leu Gly Phe Asp Asp Phe Thr Ser Ala
1155 1160 1165

CTT CAG CAT AAA GAT TAT TTA ACT CGA CGT GTT ATC GCT ACG GCA GAT
Leu Gln His Lys Asp Tyr Leu Thr Arg Arg Val Ile Ala Thr Ala Asp
1170 1175 1180

AGT ATT CCA AGG AAA CCT GGT GAA ACT GGT AAA CCA AGA AAT GGT TTG
Ser Ile Pro Arg Lys Pro Gly Glu Thr Gly Lys Pro Arg Asn Gly Leu
1185 1190 1195

CAA TCA CAA CCT TAC TTA TAC CCA AAA CCA GAG CCA TAT TTT GCA GGA
Gln Ser Gln Pro Tyr Leu Tyr Pro Lys Pro Glu Pro Tyr Phe Ala Gly
1200 1205 1210

FIG. 4 N.

CAA GAT CAT TGT AAT TAT CAA GGT AGC TCC TCT AAT TAC AGA GAC TGT
Gln Asp His Cys Asn Tyr Gln Gly Ser Ser Ser Asn Tyr Arg Asp Cys
1215 1220 1225 1230

AAA GTG CCG TTA ATT AAA GGG AA ATT TAT TAT TAT TTC GCA GCA CGC ATT
Lys Val Arg Leu Ile Lys Gly Lys Asn Tyr Tyr Phe Ala Ala Arg Asn
1235 1240 1245

AAT ATG GCA TTA GGG AAA TAC GTT GAT TTA GGT ATT CGG ATT CGG TAT
Asn Met Ala Leu Gly Lys Tyr Val Asp Leu Gly Leu Gly Ile Arg Tyr
1250 1255 1260

GAC GTA TCT CGT ACA AAA GCT AAT GAA TCA ACT ATT AGT GTT GGT AAA
Asp Val Ser Arg Thr Lys Ala Asn Glu Ser Thr Ile Ser Val Gly Lys
1265 1270 1275

TTT AAA ATT TTC TCT TGG AAT ACT GGT ATT GTC ATA AAA CCA ACG GAA
Phe Lys Asn Phe Ser Thr Asn Thr Gly Ile Val Ile Lys Pro Thr Glu
1280 1285 1290

TGG CTT GAT CCT TCT TAT CGC CTT TCT ACT GGA TTT AGA AAT CCT AGT
Trp Leu Asp Leu Ser Tyr Arg Leu Ser Thr Gly Phe Arg Asn Pro Ser
1295 1300 1305 1310

FIG. 40.

TTT TCT GAA ATG TAT CGT TCG CCG TAT CGT CGC AAG AAT GAC GAG GGT
Phe Ser Glu Met Tyr Gly Trp Arg Tyr Gly Gly Lys Asn Asp Glu Val
1315 1320 1325

TAT GTA GGT AAA TTT AAG CCT GAA ACA TCT CGT AAC CAA GAG TTT GGT
Tyr Val Gly Lys Phe Lys Pro Glu Thr Ser Arg Asn Gln Glu Phe Gly
1330 1335 1340

CTC GCT CTA AAA GGG GAT TTT CGT ATT GAG ATC AGT CAT TTT AGT
Leu Ala Leu Lys Gly Asp Phe Gly Asn Ile Glu Ile Ser His Phe Ser
1345 1350 1355

AAT GCT TAT CGA AAT CTT ATC GCC TTT GCT GAA GAA CTT AGT AAA AAT
Asn Ala Tyr Arg Asn Leu Ile Ala Phe Ala Glu Glu Leu Ser Lys Asn
1360 1365 1370

GGA ACT GGA AAG GGC AAT TAT GGA TAT CAT AAT GCA CAA AAT GCA AAA
Gly Thr Gly Lys Gly Asn Tyr Gly Tyr His Asn Ala Gln Asn Ala Lys
1375 1380 1385

TTA GTT GGC GTA AAT ATA ACT GCA CAA TTA GAT TTT AAT GGT TTA TGG
Leu Val Gly Val Asn Ile Thr Ala Gln Leu Asp Phe Asn Gly Leu Trip
1395 1400 1405

FIG. 4 P.

AAA CGT ATT CCC TAC CGT TCG TAT GCA ACA TTT GCT TAT AAC CAA GTA
Lys Arg Ile Pro Tyr Gly Trp Tyr Ala Thr Phe Ala Tyr Asn Gln Val
1410 1420

AAA GTT AAA GAT CAA AAA ATC AAT GCT GGT TTA GCC TCC GTA AGC AGT
Lys Val Lys Asp Gln Lys Ile Asn Ala Gly Leu Ala Ser Val Ser Ser
1425 1430 1435

TAT TTA TTT GAT GCC ATT CAG CCC ACC CGT TAT ATC ATT GGT TTA GCC
Tyr Leu Phe Asp Ala Ile Gln Pro Ser Arg Tyr Ile Ile Gly Leu Gly
1440 1445 1450

TAT GAT CAT CCA AGT AAT ACT TGG GGA ATT AAT ACA ATG TTT ACT CAA
Tyr Asp His Pro Ser Asn Thr Trp Gly Ile Asn Thr Met Phe Thr Gln
1455 1460 1465

TCA AAA GCA AAA TCT CAA AAT GAA TTG CTA GGA AAA CGT GCA TTA GGT
Ser Lys Ala Lys Ser Gln Asn Glu Leu Leu Gly Lys Arg Ala Leu Gly
1475 1480 1485

AAC AAT TCA ACG GAT GTA AAA TCA ACA ACA AAA CTT ACT CGG GCA TCG
Asn Asn Ser Arg Asp Val Lys Ser Thr Arg Lys Leu Thr Arg Ala Trp
1490 1495 1500

FIG. 4 Q.

CAT ATC TTA GAT GTA TCG CGT TAT TAC ATG GCG AAT AAA AAT ATT ATG
His Ile Leu Asp Val Ser Gly Tyr Tyr Met Ala Asn Lys Asn Ile Met
1505 1510

CTT CGA TTA GGG ATA TAT AAT TTA TTC AAC TAT CGC TAT GTT ACT TGG
Leu Arg Leu Gly Ile Tyr Asn Leu Phe Asn Tyr Arg Tyr Val Thr Trp
1520 1525 1530

GAA GCG GTG CGT CAA ACA GCA CAA CGT GTC AAT CAA CAT CAA AAT
Glu Ala Val Arg Gln Thr Ala Gln Gly Ala Val Asn Gln His Gln Asn
1535 1540 1545 1550

GTT CGT AGC TAT ACT CGC TAC GCA GCA TCA CGA CGA AAC TAT ACC TTA
Val Gly Ser Tyr Thr Arg Tyr Ala Ala Ser Gly Arg Asn Tyr Thr Leu
1555 1560 1565 1570

ACA TTA GAA ATG AAA TTC TAAATTAAA TGGCCAGAT GGACTAGATA
Thr Leu Glu Met Lys Phe
1570

TGCTATATCT ATACCTACT GGGCATCTT TTTCTGTCTT ATAATCTGCTT TAAGTCAAAA

ACCAACTG GATTTTAC AAGATCTTTT CACACATTAA TTG

FIG. 5 A.

ATTTGTTA CGCCATTCTT CATATTAT CCATGAACTT AAAAAACTCT AACTTGACAT

TATTACAAA AAAGATCAAT ^{-10'} ~~AATGCCATT~~ ATTATCATT ^{-35'} ~~TGTATGAGT~~ ATATAATTCT

ATG AAA TCT GAA CCT CTT ATC TCT GGT GCA CTT TCC TTT TTA CTA AGT
Met Lys Ser Val Pro Leu Ile Ser Gly Gly Leu Ser Phe Leu Leu Ser
1 5 10 15

GCT TGT ACC GCA CGG CGG TCT TTT GAT GTA GAT AAC GTC TCT AAT ACC
Ala Cys Ser Gly Gly Ser Phe Asp Val Asp Asn Val Ser Asn Thr
20 25 30

CCC TCT TCT AAA CCA CGT TAT CAA GAC GAT ACC TCG AAT CAA AGA AAA
Pro Ser Ser Lys Pro Arg Tyr Gln Asp Asp Thr Ser Asn Gln Arg Lys
35 40 45

AAA TCT AAT TTG AAA AAG TTG TTG ATT CCT TCT TTA GGA GGA GGG ATG
Lys Ser Asn Leu Lys Lys Leu Phe Ile Pro Ser Leu Gly Gly Gly Met
50 55 60

AAA TTG GTG GCT CAG AAT CTT CGT GGT AAT AAA GAA CCT AGT TTC TTA
Lys Leu Val Ala Gln Asn Leu Arg Gly Asn Lys Glu Pro Ser Phe Leu
75 80

FIG. 5B.

ATG GAA GAT GAC TAT ATA TCA TAT TTT TCC TCA CTT TCT ACG ATT GAA
Asn Glu Asp Asp Tyr Ile Ser Tyr Phe Ser Ser Leu Ser Thr Ile Glu
85 90 95

AAG GAT GTT AAA GAT AAC AAT AAA AAC GGG GCG GAC CTT ATT GGC TCA
Lys Asp Val Lys Asp Asn Asn Lys Asn Gly Ala Asp Leu Ile Gly Ser
100 105 110

ATA GAC GAG CCT AGT ACA ACA AAT CCA CCC GAA AAG CAT CAT GCA CAA
Ile Asp Glu Pro Ser Thr Thr Asn Pro Pro Glu Lys His His Gly Gln
115 120 125

AAA TAT GTA TAT TCA GGG CTT TAT TAT ACT CCA TCG TCG AGT TTA AAC
Lys Tyr Val Tyr Ser Gly Leu Tyr Thr Pro Ser Thr Ser Leu Asn
130 135 140

GAT TCT AAA AAC AAG TTT TAT TTA GGT TAC TAT GGA TAT GCG TTT TAT
Asp Ser Lys Asn Lys Phe Tyr Leu Gly Tyr Tyr Gly Tyr Ala Phe Tyr
145 150 155 160

TAT GGT AAT AAA ACT GCA ACA AAC TTG CCA GTC AAC GGT GTC GCT AAA
Tyr Gly Asn Lys Thr Ala Thr Asn Leu Pro Val Asn Gly Val Ala Lys
165 170 175

FIG. 5 C.

TAC AAA CGA ACT TGG GAT TTC ATC ACT GCA ACT AAA AAT CGC AAA CGT
Tyr Lys Gly Thr Trp Asp Phe Ile Thr Ala Thr Lys Asn Gly Lys Arg
180 185 190

TAT CCT TTG TTA AGT ATT GGC AGT CAC GCT TAT TAT CGA CGT AGT GCA
Tyr Pro Leu Ser Asn Gly Ser His Ala Tyr Tyr Arg Arg Ser Ala
195 200 205

ATT CCA GAA GAT ATT GAT TTA GAA ATT GAT TCA AAG AAT GGT GAT ATA
Ile Pro Glu Asp Ile Asp Leu Glu Asn Asp Ser Lys Asn Gly Asp Ile
210 215 220

GCG TTA ATA AGT GAA TTT AGT GCA GAT TTT GGG ACT AAA AAA CTG ACA
Gly Leu Ile Ser Glu Phe Ser Ala Asp Phe Gly Thr Lys Lys Leu Thr
225 230 235 240

GCA CAA CTG TCT TAC ACC AAA AGA AAA ACT AAT AAT CAA CCA TAT GAA
Gly Gln Leu Ser Tyr Thr Lys Arg Lys Thr Asn Asn Gln Pro Tyr Glu
245 250 255

AGG AAA AAA CTG TAT GAT ATA GAT GCC GAT ATT TAT AGT ATT AGA AGA TTC
Lys Lys Leu Tyr Asp Ile Asp Ala Asp Ile Tyr Ser Asn Arg Phe
260 265 270

FIG. 5D.

ACG GGT ACA GTA AAG CCA ACC GAA AAA GAT TCT GAA GAA CAT CCC TTT
Arg Gly Thr Val Lys Pro Thr Glu Lys Asp Ser Glu Glu His Pro Phe
275 280 285

ACC AGC GAG GGA ACA TTA GAA GGT GGT TTT TAT GGG CCT AAT GCT GAA
Thr Ser Glu Gly Thr Leu Glu Gly Phe Tyr Gly Pro Asn Ala Glu
290 295 300

CAA CTA CGG CGG AAA TTT TTA CCT ACG GAT AAC CGA GTT TTT CGG GAA
Glu Leu Gly Phe Lys Leu Ala Thr Asp Asn Arg Val Phe Gly Val
305 310 315

TTT AGT GCC AAA GAA ACG GAA ACA AAA AAG GAA GCG TTA TCC AAG
Phe Ser Ala Lys Glu Thr Glu Glu Thr Lys Glu Ala Leu Ser Lys
325 330 335

GAA ACC TTA ATT GAT CGC AAG CTA ATT ACT TTC TCT ACT AAA AAA ACC
Glu Thr Leu Ile Asp Gly Lys Leu Ile Thr Phe Ser Thr Lys Lys Thr
340 345 350

GTAT GCA AAA ACC AAT GCA ACA ACC AGT ACC GCA GCT AAT ACA ACA ACC
Asp Ala Lys Thr Asn Ala Thr Thr Ser Thr Ala Ala Asn Thr Thr Thr
355 360 365

FIG. 5E.

GAT ACA ACC GCC AAT ACA ATA ACC GAT GAA AAA AAC TTT AAG ACG GAA
Asp Thr Thr Ala Asn Thr Ile Thr Asp Glu Lys Asn Phe Lys Thr Glu
370
380

GAT ATA TCA AGT TTT GGT GAA CCT GAT TAT CTG TTA ATT GAC AAA TAT
Asp Ile Ser Ser Phe Gly Glu Ala Asp Tyr Leu Ile Asp Lys Tyr
385
390
395
400

CCT ATT CCA CCT TTA CCT GAT AAA AAT ACT AAT GAT TTC ATA AGT AGT
Pro Ile Leu Pro Asp Lys Asn Thr Asn Asp Phe Ile Ser Ser
405
410
415

AAG CAT CAT ACT GTA GGA AAT AAA CGC TAT AAA GTG GAA GCA TGT TGC
Lys His His Thr Val Gly Asn Lys Arg Tyr Lys Val Glu Ala Cys Cys
420
425
430

AGT AAT CTA AGC TAT GTG AAA TTT GGT ATG TAT TAT GAA GAC CCA CTT
Ser Asn Leu Ser Tyr Val Lys Phe Gly Met Tyr Tyr Glu Asp Pro Leu
435
440
445

AAA GAA AAA GAA ACA GAA ACA GAA ACA GAA ACA GAA AAA GAC AAA GAA
Lys Glu Lys Glu Thr Glu Thr Glu Thr Glu Thr Glu Lys Asp Lys Glu
450
455
460

FIG. 5F.

AAA GAA AAA GAA GAC AAA GAC AAA GAA AAA CAA ACG GCG GCA ACG
Lys Glu Lys Glu Lys Asp Lys Glu Lys Glu Lys Gln Thr Ala Ala Thr
465 470 475 480

ACC AAC ACT TAT CAA TTC TTA TTA CGT CAC CGT ACT CCC AAG GAC
Thr Asn Thr Tyr Tyr Gln Phe Leu Gly His Arg Thr Pro Lys Asp
485 490 495

GAC ATA CCT AAA ACA GCA AGT CCA AAA TAT CAT CGT AGT TCG TTT CGT
Asp Ile Pro Lys Thr Gly Ser Ala Lys Tyr His Gly Ser Ile Phe Gly
500 505 510

TAT ATT ACT GAC GGT AAG ACA TCT TAC TCC CCC AGT GGT GAT AAG AAA
Tyr Ile Thr Asp Gly Lys Thr Ser Tyr Ser Pro Ser Gly Asp Lys Lys
515 520 525

CCG GAT AAA AAT CCT GTC GGC GAG TTT AAT GTT GAT TTT GCC GAG AAA
Arg Asp Lys Asn Ala Val Ala Glu Phe Asn Val Asp Phe Ala Glu Lys
530 535 540

AGG CTA ACA GGC GAA TTA AAA CGA CAC GAT ACT CGA AAT CCC GTT TTT
Lys Leu Thr Gly Glu Leu Lys Arg His Asp Thr Gly Asn Pro Val Phe
545 550 555 560

FIG. 5 G.

AGT ATT GAG GCA AAC TTT AAT AAT AGT AGT AAT CCA TTC ACT GGT ACA
Ser Ile Glu Ala Asn Phe Asn Asn Ser Ser Asn Ala Phe Thr Gly Thr

565 570

GCA ACC GCA ACA AAT TTT GTA ATA GAT GGT AAA AAT AGT CAA AAT AAA
Ala Thr Ala Thr Asn Phe Val Ile Asp Gly Lys Asn Ser Gln Asn Lys
580 585

AAT ACC CCA ATT AAT ACA ACT AAA GTA AAC GGG GCA TTT TAT CGA
Asn Thr Pro Ile Asn Ile Thr Thr Lys Val Asn Gly Ala Phe Tyr Gly
595 600 605

CCT AAG CCT TCT GAA TTA GCC CGT TAT TTC ACT TAT AAC CGA AAT TCT
Pro Lys Ala Ser Glu Leu Gly Gly Tyr Phe Thr Tyr Asn Gly Asn Ser
610 615 620

ACA GCT ACA AAT TCT GAA AGT TCC TCA ACC GTC TCT TCA TCA TCC AAT
Thr Ala Thr Asn Ser Glu Ser Ser Ser Thr Val Ser Ser Ser Ser Asn
625 630 635 640

TCA AAA AAT GCA AGA GCT GCA GTT GTC TTT GGT CGG AGA CAA CAA GTA
Ser Lys Asn Ala Arg Ala Val Val Phe Gly Ala Arg Gln Gln Val
645 650 655

FIG. 5 H.

GAA ACA ACC AAA TAATGGAATA CTAAAA ATG ACT AAA CCC TAT TTT
Glu Thr Thr Lys
660
665

CGC CTA AGT ATT ATT TCT TGT CTT ATT TCA TGC TAT GTA AAA GCA
Arg Leu Ser Ile Ser Cys Leu Ile Ser Cys Tyr Val Lys Ala
675
680

GAA ACT CAA AGT ATA AAA GAT ACA AAA GAA GCT ATA TCA TCT GAA GTG
Glu Thr Gln Ser Ile Lys Asp Thr Lys Glu Ala Ile Ser Ser Glu Val
685
690
695

GAC ACT CAA AGT ACA GAA GAT TCA GAA TTA GAA ACT ATC TCA GTC ACT
Asp Thr Gln Ser Thr Glu Asp Ser Glu Leu Glu Thr Ile Ser Val Thr
700
705
710
715

GCA GAA AAA ATA AGA GAT CGT AAA GAT GAA GTA ACT GGA CTT GGC
Ala Glu Lys Ile Arg Asp Arg Lys Asp Asn Glu Val Thr Gly Leu Gly
720
725
730

AAA ATT ATC AAA ACT AGT GAA AGT ATC AGC CGA GAA CAA GTA TTA AAT
Lys Ile Ile Lys Thr Ser Glu Ser Ile Ser Arg Glu Glu Val Val Leu Asn
735
740
745

FIG. 51.

ATT CGT GAT CTA ACA CGC TAT GAT CCA CGG ATT TCA GTT GTA GAA CAA
Ile Arg Asp Leu Thr Arg Tyr Asp Pro Gly Ile Ser Val Val Glu Gln
750 755 760

CGT CGC CGT GCA ACT TCT GCA TAT TCT ATT CGT CGT ATG GAC AGA AAT
Gly Arg Gly Ala Ser Ser Gly Tyr Ser Ile Arg Gly Met Asp Arg Asn
770 775

AGA GTT GCT TTA TTA GTA GAT CGT TTA CCT CAA ACG CAA TCT TAT GTA
Arg Val Ala Leu Val Asp Gly Leu Pro Gln Thr Gln Ser Tyr Val
780 785 790 795

GTC CAA AGC CCT TTA GTT CCT CGT TCA GCA TAT TCT GGC ACT GGT GCA
Val Gln Ser Pro Leu Val Ala Arg Ser Gly Tyr Ser Gly Thr Gly Ala
800 805 810

ATT AAT GAA ATT GAA TAT GAA AAT GTA AAG GCC GTC GAA ATA AGC AAG
Ile Asn Glu Ile Glu Tyr Glu Asn Val Lys Ala Val Glu Ile Ser Lys
815 820 825

GGG CGG AGT TCT TCT GAG TAT CGT AAT GGA GCA CTA CCT GGT TCT GTA
Gly Gly Ser Ser Glu Tyr Gly Asn Gly Ala Leu Ala Gly Ser Val
830 835 840

F16.5 J.

ACA TTT CAA AGC AAA TCA GCA GCC GAT ATC TTA GAA GGA GAC AAA TCA
Thr Phe Gln Ser Lys Ser Ala Ala Asp Ile Leu Glu Gly Asp Lys Ser
845 850 855

TGG GGA ATT CAA ACT AAA AAT GCT TAT TCA AGC AAA AAT AAA GGC TTT
Trp Gly Ile Gln Thr Lys Asn Ala Tyr Ser Ser Lys Asn Lys Gly Phe
860 865 870 875

ACC CAT TCT TTA GCT GTA GCA GGA AAA CAA CGT CGA TTT GAA GGG CTA
Thr His Ser Leu Ala Val Ala Gly Lys Gln Gly Gly Phe Glu Gly Leu
880 885 890 895

GCC ATT TAC ACT CAA CGA AAT TCA ATT GAA ACC CAA GTC CAT AAA GAT
Ala Ile Tyr Thr Gln Arg Asn Ser Ile Glu Thr Gln Val His Lys Asp
895 900 905

GCA TTA AAA GGC GTA CAA AGT TAT GAT CGA TTA ATC GCC ACA ACA GAT
Ala Leu Lys Gly Val Gln Ser Tyr Asp Arg Leu Ile Ala Thr Thr Asp
910 915 920

AAA TCT TCA CGA TAC TTT GTG ATA CAA CGT GAG TGT CCA AAT GGT GAT
Lys Ser Ser Gly Tyr Phe Val Ile Gln Gly Glu Cys Pro Asn Gly Asp
925 930 935

FIG. 5K.

GAC AAG TGT GCA GCC AAG CCA CCT GCG ACT TTA TCC ACC CAA AGC GAA
Asp Lys Cys Ala Ala Lys Pro Pro Ala Thr Leu Ser Thr Gln Ser Glu
940 945 950 955

ACC GTA AGC GTT TCA GAT TAT ACG CGG GCT AAC CGT ATC AAA CCT AAT
Thr Val Ser Val Ser Asp Tyr Thr Gly Ala Asn Arg Ile Lys Pro Asn
960 965 970

CCA ATG AAA TAT GAA AGC CAG TCT TCG TTT TTA AGA GGA GGG TAT CAT
Pro Met Lys Tyr Glu Ser Gln Ser Thr Phe Leu Arg Gly Gly Tyr His
975 980 985

TTC TCT GAA CAA CAT TAT ATT GGT ATT TTT GAA TTC ACA CAA CAA
Phe Ser Glu Gln His Tyr Ile Gly Gly Ile Phe Glu Phe Thr Gln Gln
990 995 1000

AAA TTT GAT ATC CGT GAT ATG ACA TTT CCC GCT TAT TTA AGC CCA ACA
Lys Phe Asp Ile Arg Asp Met Thr Phe Pro Ala Tyr Leu Ser Pro Thr
1005 1010 1015

GAA AGA CGG GAT GAT AGT CGT TCT TTT TAT CCA ATG CAA GAT CAT
Glu Arg Arg Asp Asp Ser Ser Arg Ser Phe Tyr Pro Met Gln Asp His
1020 1025 1030 1035

FIG. 5L.

CGT GCA TAT CAA CAT ATT GAG GAT CGC AGA GGC GTT AAA TAT GCA AGT
Gly Ala Tyr Gln His Ile Glu Asp Gly Arg Gly Val Lys Tyr Ala Ser
1040 1045 1050

GGG CTT TAT TTC GAT GAA CAC CAT AGA AAA CAG CGT GTA GGT ATT GAA
Gly Leu Tyr Phe Asp Glu His His Arg Lys Gln Arg Val Gly Ile Glu
1055 1060 1065

TAT ATT TAC GAA AAT AAC AAG AAA GCG GGC ATC ATT GAC AAA GCA GTG
Tyr Ile Tyr Glu Asn Lys Ala Gly Ile Ile Asp Lys Ala Val
1075 1080 1085

TTA AGT GCT AAT CAA CAA AAC ATC ATA CTT GAC AGT ATT ATG CGA CAT
Leu Ser Ala Asn Gln Gln Ile Ile Leu Asp Ser Tyr Met Arg His
1085 1090 1095

ACG CAT TGC AGT CTT TAT CCT AAT CCA AGT AAG AAT TGC CGC CCA ACA
Thr His Cys Ser Leu Tyr Pro Asn Pro Ser Lys Asn Cys Arg Pro Thr
1100 1105 1110

CTT GAT AAA CCT TAT TCA TAC TAT CGT TCT GAT AGA ATT GTT TAT AAA
Leu Asp Lys Pro Tyr Ser Tyr Tyr Arg Ser Asp Arg Asn Val Tyr Lys
1120 1125 1130

FIG. 5M.

GAA AAA CAT AAT ATG TTG CAA TTG AAT TTA GAG AAA AAA ATT CAA CAA
Glu Lys His Asn Met Leu Gln Leu Asn Leu Glu Lys Lys Ile Gln Gln
1135 1140 1145

AAT TGG CTT ACT CAT CAA ATT GTC TTC AAT CTT CGT TTT GAT GAC TTT
Asn Trp Leu Thr His Gln Ile Val Phe Asn Leu Gly Phe Asp Asp Phe
1150 1155 1160

ACT TCA GCG CTT CAG CAT AAA GAT TAT TTA ACT CGA CGT GTT ATC GCT
Thr Ser Ala Leu Gln His Lys Asp Tyr Leu Thr Arg Val Ile Ala
1165 1170 1175

ACG GCA GAT AGT ATT CCA AGG AAA CCT CGT GAA ACT GGT AAA CCA AGA
Thr Ala Asp Ser Ile Pro Arg Lys Pro Gly Glu Thr Gly Lys Pro Arg
1180 1185 1190 1195

AAT GGT TTG CAA TCA CAA CCT TAC TTA TAC CCA AAA CCA GAG CCA TAT
Asn Gly Leu Gln Ser Gln Pro Tyr Leu Tyr Pro Lys Pro Glu Pro Tyr
1200 1205 1210

TTT GCA GGA CAA GAT CAT TGT AAT TAT CAA CGT AGC TCC TCT AAT TAC
Phe Ala Gly Gln Asp His Cys Asn Tyr Gln Gly Ser Ser Ser Asn Tyr
1215 1220 1225

F16.5 N.

AGA GAC TGT AAA GTG CGG TTA ATT AAA GGG AAA AAT TAT TAT TIC GCA
Arg Asp Cys Lys Val Arg Leu Ile Lys Gly Lys Asn Tyr Tyr Phe Ala
1230 1240

CCA CGC AAT AAT ATG GCA TTA GGG AAA TAC GTT GAT TTA CGT TTA CGT
Ala Arg Asn Asn Met Ala Leu Gly Lys Tyr Val Asp Leu Gly Leu Gly
1245 1250

ATT CGG TAT GAC GIA TCT CGT ACA AAA GCT AAT GAA TCA ACT ATT AGT
Ile Arg Tyr Asp Val Ser Arg Thr Lys Ala Asn Glu Ser Thr Ile Ser
1260 1265

GTT GGT AAA TTT AAA AAT TTC TCT TCT TGG AAT ACT GGT ATT GTC ATA AAA
Val Gly Lys Phe Lys Asn Phe Ser Thr Asn Thr Gly Ile Val Ile Lys
1280 1285

CCA ACC GAA TCG CTT GAT CTT TCT TAT CGC CTT TCT ACT GCA TTT AGA
Pro Thr Glu Trp Leu Asp Leu Ser Tyr Arg Leu Ser Thr Gly Phe Arg
1295 1300

AAT CCT AGT TTT TCT GAA ATG TAT GGT TGG CGG TAT GGT CGC AAG AAT
Asn Pro Ser Phe Ser Glu Met Tyr Gly Trp Arg Tyr Gly Gly Lys Asn
1310 1320

FIG. 50.

GAC GAG GTT TAT GTA GGT AAA TTT AAG CCT GAA ACA TCT CGT AAC CAA
Asp Glu Val Tyr Val Gly Lys Phe Lys Pro Glu Thr Ser Arg Asn Gln
1325 1330 1335

GAG TTT CGT CTC GCT CTA AAA CGG GAT TTT CGT AAT ATT GAG ATC ACT
Glu Phe Gly Leu Ala Leu Lys Gly Asp Phe Gly Asn Ile Glu Ile Ser
1340 1345 1350 1355

CAT TTT AGT AAT GCT TAT CGA AAT CTT ATC GCC TTT GCT GAA GAA CTT
His Phe Ser Asn Ala Tyr Arg Asn Leu Ile Ala Phe Ala Glu Glu Leu
1360 1365 1370 1375

AGT AAA AAT GGA ACT GGA AAG GGC AAT TAT GGA TAT CAT AAT GCA CAA
Ser Lys Asn Gly Thr Gly Lys Gly Asn Tyr Gly Tyr His Asn Ala Gln
1380 1385 1390 1395

AAT GCA AAA TTA GTT GGC GTA AAT ATA ACT GCA CAA TTA GAT TTT AAT
Asn Ala Lys Leu Val Gly Val Asn Ile Thr Ala Gln Leu Asp Phe Asn
1390 1395 1400 1405

GGT TTA TGG AAA CGT ATT CCC TAC GGT TCG TAT GCA ACA TTT GCT TAT
Gly Leu Trp Lys Arg Ile Pro Tyr Gly Trp Tyr Ala Thr Phe Ala Tyr
1410 1415

FIG. 5 P.

AAC CAA GTA AAA GTT AAA GAT CAA AAA ATC AAT GCT GGT TTA GCC TCC
Asn Gln Val Lys Val Lys Asp Gln Lys Ile Asn Ala Gly Leu Ala Ser
1420 1425 1430 1435

GTA ACC AGT TAT TTA TTT GAT GCC ATT CAG CCC AGC CGT TAT ATC ATT
Val Ser Ser Tyr Leu Phe Asp Ala Ile Gln Pro Ser Arg Tyr Ile Ile
1440 1445 1450 1455

GGT TTA GGC TAT GAT CCA AGT AAT ACT TGG GGA ATT AAT ACA ATG
Gly Leu Gly Tyr Asp His Pro Ser Asn Thr Trp Gly Ile Asn Thr Met
1460 1465 1470 1475

TTT ACT CAA TCA AAA GCA AAA TCT CAA AAT GAA TTG CTA GGA AAA CGT
Phe Thr Gln Ser Lys Ala Lys Ser Gln Asn Glu Leu Gly Lys Arg
1480 1485 1490 1495

CCA TTA CGT AAC AAT TCA ACG GAT GTA AAA TCA ACA AGA AAA CTT ACT
Ala Leu Gly Asn Ser Arg Asp Val Lys Ser Thr Arg Lys Leu Thr
1500 1505 1510 1515

FIG. 5Q.

AT T ATG CTT CGA TTA GGG ATA TAT AAT TTA TTC AAC TAT CGC TAT
Asn Ile Met Leu Arg Leu Gly Ile Tyr Asn Leu Phe Asn Tyr Arg Tyr
1520 1530

GTT ACT TGG GAA GCG GTG CGT CAA ACA GCA CAA CGT GCG GTC AAT CAA
Val Thr Thr Glu Ala Val Arg Gln Thr Ala Gln Gly Ala Val Asn Gln
1535 1545

CAT CAA AAT GTT CGT AGC TAT ACT CGC TAC GCA GCA TCA CGA CGA AAC
His Gln Asn Val Gly Ser Tyr Thr Arg Tyr Ala Ala Ser Gly Arg Asn
1550 1560

TAT ACC TTA ACA TTA GAA ATG AAA TTC TAAATTAAA TGCGCCAGAT
Tyr Thr Leu Thr Leu Glu Met Lys Phe
1565 1570

GGACTAGATA TGCTATATCT ATACCTACT GGGCCATCTT TTCTGTCT ATAATCTGCT

TAAGTGAAA ACCAAACTG GATTITTTAC AAGATCTTTT CACACATTAA TIGTAAATC

TCGGACAAATT TIGACCCG

FIG. 6 A.

AAAATTGGT AATGATAACC CTATAATG A TAAGAGAGAA AGTGTGTTA CGCCATTIT

CATATTAT CCATGAACTT AAAAAATCTT ⁻³⁵ ~~AGTTGACAT~~ ⁻¹⁰ TATTACAAA AAAGAACAT

AATGGAAATT ATTATCAATT ^{RBS} ~~TGTTATAAGT~~ ATTAAATTCTT ATG AAA TCT GTA OCT

Met Lys Ser Val Pro
1 5

CTT ATC ACT GGT GGA CTT TCC TTT TTA CTA AGC GCT TGT AGC GGG GGA
Leu Ile Thr Gly Leu Ser Phe Leu Ser Ala Cys Ser Gly Gly
10 15 20

GGT GGT TCT TTT GAT GTA GAT GAC GTC TCT AAT CCC TCC TCT TCT AAA
Gly Gly Ser Phe Asp Val Asp Val Ser Asn Pro Ser Ser Ser Lys
25 30 35

CCA CGT TAT CAA GAC GAT ACC TCG AAT CAA AGA ACA AAA TCT GAT TTG
Pro Arg Tyr Gln Asp Asp Thr Ser Asn Gln Arg Thr Lys Ser Asp Leu
40 45 50

GAA AAG TTG TTC ATT CCT TCT TTA GGG GGA GGG ATG AAG TTA GTG GCT
Glu Lys Leu Phe Ile Pro Ser Leu Gly Gly Met Lys Leu Val Ala
55 60 65

FIG. 6B.

CAA AAT TTT ATT GGT GCT AGA GAA CCT AGT TTC TTA AAT GAA GAT GGC
Gln Asn Phe Ile Gly Ala Arg Glu Pro Ser Phe Leu Asn Glu Asp Gly
70 75 80 85

TAT ATG ATA TTT TCC TCA CTT TCT ACG ATT GAA GAG GAT GTT GAA AAA
Tyr Met Ile Phe Ser Ser Leu Ser Thr Ile Glu Glu Asp Val Glu Lys
90 95 100

GTT AAA AAT AAC AAT AAA AAC CGG CGG CGG CTT ATT GCC TCA ATT GAG
Val Lys Asn Asn Lys Asn Gly Gly Arg Leu Ile Gly Ser Ile Glu
105 110 115

GAA CCT AAT GCA ACA TCA CAA AAT TCT AAT TCA CAA GAA TAC GTT TAT
Glu Pro Asn Gly Thr Ser Gln Asn Ser Asn Ser Gln Glu Tyr Val Tyr
120 125 130

TCT GGT TTG TAT ATC GAT AGT TGG CGT GAT TAT AAG AAG GAA GAG
Ser Gly Leu Tyr Tyr Ile Asp Ser Thr Arg Asp Tyr Lys Lys Glu Glu
135 140 145

CAA AAA GCT TAT ACT GCC TAT TAT GCA TTT TAT TAT GGT AAT
Gln Lys Ala Tyr Thr Gly Tyr Tyr Ala Phe Tyr Tyr Gly Asn
155 160 165

FIG. 6C.

GAA ACT GCA AAA AAC TTG CCA GTA AAA GGT GTA GCT AAA TAC AAA CGA
Glu Thr Ala Lys Asn Leu Pro Val Lys Gly Val Ala Lys Tyr Lys Gly
170 175 180

ACG TGG AAC TTC ATC ACT GCA ACT GAA MAT CGC AAA CGT TAT TCT TTG
Thr Trp Asn Phe Ile Thr Ala Thr Glu Asn Gly Lys Arg Tyr Ser Leu
185 190 195

TTC AGT AAT TCT ATC GGT CAA GCT TAT TCC AGA CGC AGC GCT ATT TCA
Phe Ser Asn Ser Ile Gly Gln Ala Tyr Ser Arg Arg Ser Ala Ile Ser
200 205 210

GAA GAT ATC TAT AAT TTA GAA AAC GGT GAC GCG GCG TTA ATA AGT GAA
Glu Asp Ile Tyr Asn Leu Glu Asn Gly Asp Ala Gly Leu Ile Ser Glu
215 220 225

TTT AGT GTA GAT TTT CGT AAG AAA CGG CTC ACT GCA GAA CCT TAT TAT
Phe Ser Val Asp Phe Gly Lys Lys Glu Leu Thr Gly Glu Leu Tyr Tyr
230 235 240 245

AAT GAA AGG AAA ACA AGT GTT AAT GAA TCA CAA AAT ACA ACA CAT AAA
Asn Glu Arg Lys Thr Ser Val Asn Glu Ser Gln Asn Thr Thr His Lys
250 255 260

FIG. 6D.

CTC TAC ACT CTA GAA GCT AAA GTG TAT AGC AAC CGA TTC AGA GGT AAA
Leu Tyr Thr Leu Glu Ala Lys Val Tyr Ser Asn Arg Phe Arg Gly Lys
270 275

GTA AAG CCA ACC AAA ACA AAG TCT GAA GAT CAT CCC TTT ACC AGC GAG
Val Lys Pro Thr Lys Thr Lys Ser Glu Asp His Pro Phe Thr Ser Glu
285 290

CGA ACA TTA GAA CGT CGT TTT TAT CGG CCT AAT CCT GAA GAA CTA CGG
Gly Thr Leu Glu Gly Phe Tyr Gly Pro Asn Ala Glu Glu Leu Gly
295 300 305

GGA AAG TTT TTA GCT AAC GAC GAA AAA GTT TTT CGG GTA TTT AGT GCC
Gly Lys Phe Leu Ala Asn Asp Glu Lys Val Phe Gly Val Phe Ser Ala
310 315 320 325

AAA GAA GAC CCA CAA AAC CCA GAA AAC CAA AAA TTA TCC ACA GAA ACC
Lys Glu Asp Pro Gln Asn Pro Glu Asn Gln Lys Leu Ser Thr Glu Thr
330 335 340

TTA ATT GAT CGC AAG CTA ATT ACT TTT AAA AGA ACT GAT GCA ACA ACC
Leu Ile Asp GLY Lys Leu Ile Thr Phe Lys Arg Thr Asp Ala Thr Thr
345 350 355

FIG. 6E.

AAT GCA ACA ACC GAT GCA AAA ACC AGT GCA ACA ACC GAT GCA ACC AGT
Asn Ala Thr Thr Asp Ala Lys Thr Ser Ala Thr Thr Asp Ala Thr Ser
360 365 370

ACA ACA GCC AAT AAA AAA ACC GAT GCA GAA AAC TTT AAG ACG GAA GAT
Thr Thr Ala Asn Lys Lys Thr Asp Ala Glu Asn Phe Lys Thr Glu Asp
375 380 385

ATA CCA AGT TTT CGT GAA GCT GAT TAC CTT TTA ATT CGC AAT CAG CCT
Ile Pro Ser Phe Gly Glu Ala Asp Tyr Leu Leu Ile Gly Asn Gln Pro
390 395 400 405

ATT CCT CTT TTA CCT GAA AAA AAT ACT GAT GAT TTC ATA AGT AGT AAG
Ile Pro Leu Leu Pro Glu Lys Asn Thr Asp Asp Phe Ile Ser Ser Lys
410 415 420

CAC CAT ACG GTA CGA CGT AAA ACC TAT AAA GTA GAA GCA TGT TGC AAG
His His Thr Val Gly Gly Lys Thr Tyr Lys Val Glu Ala Cys Cys Lys
425 430 435

AAT CTA AGC TAT GTG AAA TTT CGT ATG TAT TAT GAG GAT AAA GAT AAG
Asn Leu Ser Tyr Val Lys Phe Gly Met Tyr Tyr Glu Asp Lys Asp Lys
440 445 450

FIG. 6F.

GAC AAC AAA AAT GAA ACA GAC AAA GAA AAA GGC AAA GAA AAA CCA ACG
Asp Asn Lys Asn Glu Thr Asp Lys Glu Lys Gly Lys Glu Lys Pro Thr
460
465

ACG ACA ACA TCT ATC AAC ACT TAT TAT CAA TTC TTA TTA CGT CTC CTC CGT
Thr Thr Ser Ile Asn Thr Tyr Tyr Gln Phe Leu Leu Gly Leu Arg
470
475
480
485

ACT CCC AAG GAC GAA ATA CCT AAA GAA GGA AGT GCA AAA TAT CAT CGT
Thr Pro Lys Asp Glu Ile Pro Lys Glu Gly Ser Ala Lys Tyr His Gly
490
495
500

AAT TGG TTT GGT TAT ATT AGT GAT GGC GAG ACA TCT TAC TCC GCC AGT
Asn Trp Phe Gly Tyr Ile Ser Asp Gly Glu Thr Ser Tyr Ser Ala Ser
505
510
515

GGT GAT AAG GAA CGC AGT AAA AAT GCT GTC GCC GAG TTT GAT GTA AGT
Gly Asp Lys Glu Arg Ser Lys Asn Ala Val Ala Glu Phe Asp Val Ser
520
525
530

TTT GCC AAT AAA ACA TTA ACA GGC GAA TTA AAA CGA CAC GAT AAT GGA
Phe Ala Asn Lys Thr Leu Thr Gly Glu Leu Lys Arg His Asp Asn Gly
535
540
545

FIG. 6 G.

AAT ACC GTA TTT AAA ATT AAT GCA GAA TTA AAT GGT AGT AAT GAC GTC
Asn Thr Val Phe Lys Ile Asn Ala Glu Leu Asn Gly Ser Asn Asp Phe
550 555 560 565

ACT GGT ACA GCA ACC GCA ACA AAT TTT GTA ATA GAT GGT AAC AAT AGT
Thr Gly Thr Ala Thr Asn Ile Val Ile Asp Gly Asn Asn Ser
570 575 580

CAA ACT TCA AAT GCC AAA ATT AAT ACA ACT AAA GTA AAT GGG GCA
Gln Thr Ser Asn Ala Lys Ile Asn Ile Thr Thr Lys Val Asn Gly Ala
585 590 595

TTC TAT GGA CCT AAG GCT TCT GAA TTA GGA GGG TAT TTC ACC TAT AAC
Phe Tyr Gly Pro Lys Ala Ser Glu Leu Gly Gly Tyr Phe Thr Tyr Asn
600 605 610

GGA AAA AAT CCT ACA GCT ACA AAT TCT GAA AGT TCC TCA ACC GTA CCT
Gly Lys Asn Pro Thr Ala Thr Asn Ser Glu Ser Ser Ser Thr Val Pro
615 620 625

TCA CCA CCC AAT TCA CCA AAT GCA AGC GCT GCA GTT GTC TTT CGT GCT
Ser Pro Pro Asn Ser Pro Asn Ala Ser Ala Ala Val Val Phe Gly Ala
630 635 640 645

FIG. 6H.

AAA AAA CAA GTA GAA ACA ACC AAC AAG TAAAAAAC CAAGTAATGG
Lys Lys Gln Val Glu Thr Thr Asn Lys
650

AATACTAAAATG ACT AAA AAA CCC TAT TTT CGC CTA AGT ATT ATT TCT
Met Thr Lys Lys Pro Tyr Phe Arg Leu Ser Ile Ile Ser
655
660
665

TGT CTT TTA ATT TCA TGC TAT GTA AAA GCA GAA ACT CAA AGT ATA AAA
Cys Leu Ile Ser Cys Tyr Val Lys Ala Glu Thr Gln Ser Ile Lys
670
675
680

GAT ACA AAA GAA GCT ATA TCA TCT GAA GTG GAC ACT CAA AGT ACA GAA
Asp Thr Lys Glu Ala Ile Ser Ser Glu Val Asp Thr Gln Ser Thr Glu
685
690
695

GAT TCA GAA TTA GAA ACT ATC TCA GTC ACT GCA GAA ATA AGA GAT
Asp Ser Glu Leu Glu Thr Ile Ser Val Thr Ala Glu Lys Ile Arg Asp
700
705
710
715

CGT AAA GAT AAT GAA GTA ACT GGA CTT GGC AAA ATT ATC AAA ACT AGT
Arg Lys Asp Asn Glu Val Thr Gly Leu Gly Lys Ile Lys Thr Ser
725
730

FIG. 61.

GAA AGT ATC AGC CGA GAA CAA GTA TTA AAT ATT CGT GAT CTA ACA CGC
Glu Ser Ile Ser Arg Glu Gln Val Leu Asn Ile Arg Asp Leu Thr Arg
745

TAT GAT CCA CGC ATT TCA GTT GTA GAA CAA CGC CGT GGT GCA AGT TCT
Tyr Asp Pro Gly Ile Ser Val Val Glu Gln Gly Arg Gly Ala Ser Ser
750 755

CGA TAT TCT ATT CGT GGT ATG GAC AGA AAT AGA GTT GCT TTA TTA GTA
Gly Tyr Ser Ile Arg Gly Met Asp Arg Asn Arg Val Ala Leu Leu Val
765 770 775

GAT GGT TTA CCT CAA ACG CAA TCT TAT GTA GTG CAA AGC CCT TTA GTT
Asp Gly Leu Pro Gln Thr Gln Ser Tyr Val Val Gln Ser Pro Leu Val
780 785

CCT CGT TCA CGA TAT TCT CGC ACT GGT GCA ATT AAT GAA ATT GAA TAT
Ala Arg Ser Gly Tyr Ser Gly Thr Gly Ala Ile Asn Glu Ile Glu Tyr
800 805

GAA AAT GTA AAG GCC GTC GAA ATA AGC AAG GGG GGG AGT TCT TCT GAG
Glu Asn Val Lys Ala Val Glu Ile Ser Lys Gly Gly Ser Ser Ser Glu
820 825

FIG. 6J.

TAT CGT AAT GGA GCA CTA GCT CGT TCT GTA ACA TTT CAA AGC AAA TCA
Tyr Gly Asn Gly Ala Ile Ala Gly Ser Val Thr Phe Gln Ser Lys Ser
830 835

GCA GCC GAT ATC TTA GAA CGA GAC AAA TCA TCG GGA ATT CAA ACT AAA
Ala Ala Asp Ile Leu Glu Gly Asp Lys Ser Thr Gly Ile Gln Thr Lys
845 850

AAT GCT TAT TCA AGC AAA AAT AAA GGC TTT ACC CAT TCT TTA GCT GTA
Asn Ala Tyr Ser Ser Lys Asn Lys Gly Phe Thr His Ser Ile Ala Val
860 865

GCT GGA AAA CAA CGG CGA TTT GAC GGG GTC GCC ATT TAT ACT CAA CGA
Ala Gly Lys Gln Gly Gly Phe Asp Gly Val Ala Ile Tyr Thr Gln Arg
880 885

AAT TCA ATT GAA ACC CAA GTC CAT AAA GAT GCA TTA AAA GGC GTA CAA
Asn Ser Ile Glu Thr Gln Val His Lys Asp Ala Leu Lys Gly Val Gln
900 905

AGT TAT CAT CGA TTA ATC GCC AAA CCA GAG GAT CAA TCT GCA TAC TTT
Ser Tyr His Arg Leu Ile Ala Lys Pro Glu Asp Gln Ser Ala Tyr Phe
910 915

FIG. 6K.

GTG ATG CAA GAT GAG TGT CCA AGC CCA GAT GAT TAT AAC AGT TGT TTA
Val Met Gln Asp Glu Cys Pro Lys Pro Asp Asp Tyr Asn Ser Cys Leu
925 930 935

CCT TTC GCC AAA CGA CCT GCG ATT TTA TCC TCC CAA AGA GAA ACC GTA
Pro Phe Ala Lys Arg Pro Ala Ile Leu Ser Ser Gln Arg Glu Thr Val
940 945 950 955

AGC GTT TCA GAT TAT ACG GGG GCT AAC CGT ATC ATC AAA CCT AAT CCA ATG
Ser Val Ser Asp Tyr Thr Gly Ala Asn Arg Ile Lys Pro Asn Pro Met
960 965 970

AAA TAT GAA ACC CAG TCT TCG TTT TTA AGA GCA CGG TAT CAT TTT TCT
Lys Tyr Glu Ser Gln Ser Thr Phe Leu Arg Gly Gly Tyr His Phe Ser
975 980 985

GAA CAA CAT TAT ATT GGT ATT TTT GAA TTC ACA CAA CAA AAA TTT
Glu Gln His Tyr Ile Gly Ile Phe Glu Phe Thr Gln Gln Lys Phe
990 995 1000

GAT ATC CGT GAT ATG ACA TTT CCC GCT TAT TTA AGA TCA ACA GAA AAA
Asp Ile Arg Asp Met Thr Phe Pro Ala Tyr Leu Arg Ser Thr Glu Lys
1005 1010 1015

FIG. 6L.

CGG GAT GAT AGC AGT GGC TCT TTT TAT CCA AAG CAA GAT TAT CGT GCA
Arg Asp Asp Ser Ser Gly Ser Phe Tyr Pro Lys Gln Asp Tyr Gly Ala
1020 1025 1030 1035

TAT CAA CGT ATT GAG GAT GGC CCA GGC GTT AAC TAT GCA AGT GGG CTT
Tyr Gln Arg Ile Glu Asp Gly Arg Gly Val Asn Tyr Ala Ser Gly Leu
1040 1045 1050 1055

TAT TTC GAT GAA CAC CAT AGA AAA CAG CGT GTA GGT ATT GAA TAT ATT
Tyr Phe Asp Glu His His Arg Lys Gln Arg Val Gly Ile Glu Tyr Ile
1060 1065 1070 1075

TAC GAA AAT AAG AAC AAA GCG GCG ATC ATT GAC AAA GCA GTG TTA AGT
Tyr Glu Asn Lys Ala Gly Ile Ile Asp Lys Ala Val Leu Ser
1080 1085 1090 1095

GCT AAT CAA CAA AAC ATC ATA CTT GAC AGT TAT ATG CAA CAT ACG CAT
Ala Asn Gln Gln Asn Ile Ile Leu Asp Ser Tyr Met Gln His Thr His
1085 1090 1095 1100

TGC AGT CCT TAT CCT AAT CCA AGT AAG AAT TGC CGC CCA ACA CGT GAT
Cys Ser Leu Tyr Pro Asn Pro Ser Lys Asn Cys Arg Pro Thr Arg Asp
1100 1105 1110 1115

FIG. 6M.

AAA CCT TAT TCA TAC TAT CAT TCT GAT AGA AAT GTT TAT AAA GAA AAA
Lys Pro Tyr Ser Tyr Tyr His Ser Asp Arg Asn Val Tyr Lys Glu Lys
1120 1125 1130 1135

CAT AAT ATG TTG CAA TTG AAT TTA GAG AAA AAA ATT CAA CAA AAT TGG
His Asn Met Leu Gln Ile Asn Leu Glu Lys Lys Ile Gln Gln Asn Trp
1140 1145 1150

CTT ACT CAT CAA ATT GTC TTC AAT CTT GGT TTT GAT GAC TTT ACT TCA
Leu Thr His Gln Ile Val Phe Asn Leu Gly Phe Asp Asp Phe Thr Ser
1155 1160 1165

CCG CTT CAG CAT AAA CAT TAT TTA ACT CGA CGT GTT ACC GCT ACG GCA
Ala Leu Gln His Lys Asp Tyr Leu Thr Arg Val Arg Val Thr Ala Thr Ala
1170 1175 1180

AAG AGT ATT TCA GAG AAA GCT AAT GAA ACA AGA AGA AAT GGT TAC AAA
Lys Ser Ile Ser Glu Lys Ala Asn Glu Thr Arg Arg Asn Glu Gly Tyr Lys
1185 1190 1195 1200

AAA CAA CCT TAC TTA TAC CCA AAA CCA ACA GTC CGT TTT GTC GTC CAA
Lys Gln Pro Tyr Leu Tyr Pro Lys Pro Thr Val Gly Phe Val Val Gln
1205 1210

FIG. 6N.

GAT CAT TGT GAT TAT AAA GGT AAC TCC TCT AAT TAC AGA GAC TGT AAA
Asp His Cys Asp Tyr Lys Gly Asn Ser Ser Asn Tyr Arg Asp Cys Lys
1215 1220 1225

GTG CGG TTA ATT AAA CGG AAA AAT TAT TAT TTC GCA GCA CGC AAT AAT
Val Arg Leu Ile Lys Gly Lys Asn Tyr Tyr Phe Ala Ala Arg Asn Asn
1230 1235 1240

ATG GCA TTA CGG AAA TAC GTT GAT TTA GGT TTA GGT ATT CGG TAT GAC
Met Ala Leu Gly Lys Tyr Val Asp Leu Gly Leu Gly Ile Arg Tyr Asp
1245 1250 1255

GTA TCT CGC ACA AAA GCT AAT GAA TCA ACT ATT AGT GTT GGT AAA TTT
Val Ser Arg Thr Lys Ala Asn Glu Ser Thr Ile Ser Val Gly Lys Phe
1260 1265 1270

AAA AAT TTC TCT TGG AAT ACT GGT ATT GTC ATA AAA CCA ACG GAA TGG
Lys Asn Phe Ser Trp Asn Thr Gly Ile Val Ile Lys Pro Thr Glu Trp
1280 1285 1290

CTT GAT CTT TCT TAT CGC CTT TCT ACT GGA AAT CCT AGT TTT
Leu Asp Leu Ser Tyr Arg Leu Ser Thr Gly Phe Arg Asn Pro Ser Phe
1295 1300 1305

FIG. 60.

GCT GAA ATG TAT GGT TGG CGG TAT GGT CGC AAT AAT AGC GAG GTT TAT
Ala Glu Met Tyr Gly Trp Arg Tyr Gly Gly Asn Asn Ser Glu Val Tyr
1310 1315 1320 1325

GTA GGT AAA TTT AAG CCT GAA ACA TCT CGT AAC CAA GAG TTT GGT CTC
Val Gly Lys Phe Lys Pro Glu Thr Ser Arg Asn Gln Glu Phe Gly Leu
1330 1335 1340 1345

GCT CTA AAA CGG GAT TTT CGT AAT ATT GAG ATC AGT CAT TTT AGT AAT
Ala Leu Lys Gly Asp Phe Gly Asn Ile Glu Ile Ser His Phe Ser Asn
1340 1345 1350 1355 1360

GCT TAT CGA AAT CTT ATC GCC TTT GCT GAA GAA CTT AAT AAA AAT GGA
Ala Tyr Arg Asn Leu Ile Ala Phe Ala Glu Glu Leu Asn Lys Asn Gly
1365 1370 1375 1380

ACT GGA AAG GCC AAT TAT GGA TAT CAT AAT GCA CAA AAT GCA AAA TTA
Thr Gly Lys Ala Asn Tyr Gly Tyr His Asn Ala Gln Asn Ala Lys Leu
1385 1390 1395 1400

GTT GGC GTA AAT ATA ACT GCG CAA TTA GAT TTT AAT GGT TTA TGG AAA
Val Gly Val Asn Ile Thr Ala Gln Leu Asp Phe Asn Gly Leu Trp Lys

FIG. 6P.

CGT ATT CCC TAC CGT TGG TAT GCA ACA TTT GCT TAT AAC CGA GTA AAA
Arg Ile Pro Tyr Gly Itp Tyr Ala Thr Phe Ala Tyr Asn Arg Val Lys
1405 1410 1415

GTT AAA GAT CAA AAA ATC AAT GCT CGT TTG GCC TCC GTA AGT AGT TAT
Val Lys Asp Gln Lys Ile Asn Ala Gly Leu Ala Ser Val Ser Ser Tyr
1420 1425 1430 1435

TTA TTT GAT GCC ATT CAG CCC AGC CGT TAT ATC ATT CGT TTA GGC TAT
Leu Phe Asp Ala Ile Gln Pro Ser Arg Tyr Ile Ile Gly Leu Gly Tyr
1440 1445 1450 1455

GAT CAT CCA AGT AAT ACT TGG CGA ATT AAT ACA ATG TTT ACT CAA TCA
Asp His Pro Ser Asn Thr Itp Gly Ile Asn Thr Met Phe Thr Gln Ser
1460 1465 1470 1475

AAA GCA AAA TCT CAA AAT GAA TTG CTA GGA AAA CGT GCA TTG GGT AAC
Lys Ala Lys Ser Gln Asn Glu Leu Leu Gly Lys Arg Ala Leu Gly Asn
1480 1485 1490 1495

AAT TCA AGG GAT GTA AAA TCA ACA AGA AAA CTT ACT CGG GCA TGG CAT
Asn Ser Arg Asp Val Lys Ser Thr Arg Lys Leu Thr Arg Ala Itp His
1495 1490 1485 1480

FIG. 6Q.

ATC TTA GAT GIA TCG GGT TAT TAC ATG GCG AAT AAA AAT ATT ATG CTT
Ile Leu Asp Val Ser Gly Tyr Tyr Met Ala Asn Lys Ile Met Leu
1500 1505 1510 1515

CGA TTA CGG ATA TAT ATT TTA TTC AAC TAT CGC TAT GTT ACT TGG GAA
Arg Leu Gly Ile Tyr Asn Leu Phe Asn Tyr Arg Tyr Val Thr Trp Glu
1520 1525 1530 1535

GCG GTG CGT CAA ACA GCA CAA GGT GCG GTC AAT CAA CAT CAA AAT GTT
Ala Val Arg Gln Thr Ala Gln Gly Ala Val Asn Gln His Gln Asn Val
1540 1545 1550 1555

GGT AGC TAT ACT CGC TAC GCA GCA TCA GCA CGA AAC TAT ACC TTA ACA
Gly Ser Tyr Thr Arg Tyr Ala Ala Ser Gly Arg Asn Tyr Thr Leu Thr
1560 1565

TTA GAA ATG AAA TCTTAATTAA AAATGCCCA GATGGACTAG ACATGCTATA
Leu Glu Met Lys
1565

TCTATACCTT ACTGGGGCAT CTTTTCTGT TCTATAATCT GGTTAAGTGA AAAACCAAAC
TGGATTTTT TAGAAGATCT TICCAGGCAT TTATTGAAA ATCTCCGACA ATTTTACCG

CACTTTCTC TATTACAAA ACAATAAGGA TCTTTTGTG AAATCTCTCA

FIG. 7 A.

CAACATCTCC OCTAAGCTTATA TTGGTTAACG ATTAAGCCCAT TTATGCTGTTATG

ATAAGAAAGA AATTTCGTTT AGGCCATT TTACATATTAA TCCATGAACT TAAAAAATTTC

TAAGTTGACA TTATTACAAA AAAAGAACAA TAATGGAAAT TATTATCAAT TTGTATAAG

TTA TTA AGT GCT TGT AGC CGA CGA CGG TCT TCT TTT CAT GTA GAT AAC GTC	15	20	25
Leu Leu Ser Ala Cys Ser Gly Gly Ser Phe Asp Val Asn Val			

CAA ACA AAA TCT GAT TTG CAA AAG TTG TCC ATT CCT TCT TTA CGG
Gln Arg Thr Lys Ser Asp Leu Gln Lys Leu Ser Ile Pro Ser Leu Gly
50 55 60

FIG. 7B.

CGA GGG ATG AAG TTA GTG GCT CAG AAT CTT CTT GGT AAG AAA GAA GCT
Gly Gly Met Lys Leu Val Ala Gln Asn Leu Leu Gly Lys Lys Glu Pro
65 70 75

AGT CTC TTA AAT AAT GAA GAT GGC TAT ATG ATA TTT TCC TCA CTT TCT
Ser Leu Leu Asn Asn Glu Asp Gly Tyr Met Ile Phe Ser Ser Leu Ser
80 85 90

ACG ATT GAA GAG GAT GTT ACA AAA GAA AAT AAA TCT CAG GAA CCC ACT
Thr Ile Glu Glu Asp Val Thr Lys Glu Asn Lys Ser Gln Glu Pro Thr
95 100 105

ATT GGC TCA ATA GAC GAG CCT AGC AAA ACA AAT TCA CCC CAA AAT CAT
Ile Gly Ser Ile Asp Glu Pro Ser Lys Thr Asn Ser Pro Gln Asn His
110 115 120 125

CAT GGC AAT ATG TAT ATT CGG GTC TTT ATT ATA TTC AAT CGT GGC GTA
His Gly Asn Met Tyr Ile Arg Val Phe Ile Ile Phe Asn Arg Gly Val
130 135 140 145

ATT CCT CAA ATG GCA AGT TTT ATT CAG GTT ACT ATG GAT ATG CGT ATT
Ile Pro Gln Met Ala Ser Phe Ile Gln Val Thr Met Asp Met Arg Ile
150 155

FIG. 7 C.

ACT TTG GCA AGC AAA CAG CCA CTA CAT TAC CTG TAGATGCCA AGCAACGTAT
Thr Leu Ala Ser Lys Gln Pro Leu His Tyr Leu

160

165

AAAGGAACCTT GGCACTCTAT CACCGCAACT GAAATGGCA AAAAGTATTC TTGGTTCAGT
AATCATAGCG GTCAAGCTTA TCGCACACGT AGTGCATTTC CAGAAGATAT TGATTAGAA
AAAATGATT CAACTAATGG TGACAAAGGGC TTAATAAGTG AATTTAGTGT CAATTTCGGT
ACAAAAAGC TCACTGGAA ACTTTATTAT AATGAAAGAG AACAGAACT TAATAATCA
AAAGATACAA AACATACACT CTACATCTA GAAGCTCAAG TGTATAGTAA CCGATTCAAG
GGTACAGTAA AGCCAACCGA AAAAGATCT ACAGATCATIC CCTTACCG CGAGGAAACA
TTAGAAGGGG GTTTTATGG GCCTTAAGGT GAAGAACTAG GAGGAAAGT TTACCTGGC
CTATAAAAG TTTTGGGT ATTAGTGCC AAAGAAACGG AAGAAACAA AAAGAAAGCG
TTATCCAAGG AACCTTAAT TGATGCCAAG CTAACTACTT TTAAACAC CAATGCAACA
ACCAATGCAA CAGGCAATGCC ACAACCCAGT ACAACACCA GTACAAACAC CCATGCCAGAA

FIG. 7 D.

AACTTACCA CGAAAGATAT ACCAAGTTT GGTGAACCTG ATTACCTTT AATTGATAAT
TACCCCTGTC CCTCTTACCG TGAGAGCTGT GATTCTAA GTAGTAACCA CCATACIGTA
CGAAAGAAA CCTATCAAGT AGAACATGT TCGAGTAAATC TAAGCTATGT GAAATTGGT
ATGTTTATG AAGAACCCACT TAAGAAGAA AAAGACAAAG AAAAAGAAGA AGACAAAGAA
AACAAACGG CGCGAACCGAC CAACACTTAT TATCAATTC TATTAGGTCT CCGTACTGCC
AGTTCTGAAA TICCTAAAT GGGAAACGTG GAATATCGCG GTAATTGGTT TGTATATT
ACTGATGCCA CGACATCTTA CTCCCCAGT GGTGATAAGG AACGCAATTA AAATGCTCCC
GGCGATTTA ATGTTGATT TGTCATAAAA AAGCTAACAG CCACATTAA ACCGACCGAT
ATGGAATA CCGTATTAG TATTCAGGCA AACTTAACCA GGGGAATGA CTTCACIGGT
AAACCAACCG CAAACATT AGTAATAAGAT GTTAAAGTA CACAAGCCAC ATCTAAAGTC
AATTTCACGG CAAACAGTAAA ACCGGCATT TATGGACCTG ATGCTTCCTCA ATTAGCGGT
TATTTCACCT ATAACGGAAA AAATCTACA GCTACAAATT CCCAACCGT ATCTTCACCA

FIG. 7E.

TCCTAATTAG CAAATGCTCG TGCCTGCCGTT GTGTTTCGAG CTAAAAACA AGTACACACA

ACCAACAGT AGAAAAACC AAATAATGGA ATACTAAAAA ATG ACT AAA AAA CCC
Tyr Phe Arg Leu Ser Ile Ser Cys Leu Ile Ser Cys Tyr Val
170

TAT TTT CGC CTA AGT ATT ATT TCT TGT CTT TTA ATT TCA TGC TAT GTA
Tyr Phe Arg Leu Ser Ile Ser Cys Leu Ile Ser Cys Tyr Val
175
180

AAA GCA GAA ACT CAA AGT ATA AAA GAT ACA AAA GAA GCT ATA TCA TCT
Lys Ala Glu Thr Gln Ser Ile Lys Asp Thr Lys Glu Ala Ile Ser Ser
190
195
200

GAA GTG GAC ACT CAA AGT ACA GAA GAT TCA GAA TTA GAA ACT ATC TCA
Glu Val Asp Thr Gln Ser Thr Glu Asp Ser Glu Leu Glu Thr Ile Ser
210
215
220

GTC ACT GCA GAA AAA ATA ACA GAT CGT AAA GAT ATT GAA GAA ACT GCA
Val Thr Ala Glu Lys Ile Arg Asp Arg Lys Asp Asn Glu Val Thr Gly
225
230
235

CTT GCC AAA ATT ATA AAA ACG AGT GAA AGT ATC AGC CGA GAA CAA GTA
Leu Gly Lys Ile Ile Lys Thr Ser Glu Ser Ile Ser Arg Glu Gln Val
240
245
250

F16.7F.

TTA AAT ATT CGT GAT CTA ACA CGC TAT GAT CCA CGC ATT TCA GTT GTA
Leu Asn Ile Arg Asp Ile Thr Arg Tyr Asp Pro Gly Ile Ser Val Val
255 260 265

GAA CAA CGT CGC CGT GCA AGT TCT CGA TAT TCT ATT CGT CGT ATG GAC
Glu Gln Gly Arg Gly Ala Ser Ser Gly Tyr Ser Ile Arg Gly Met Asp
270 275 280 285

AGA AAT AGA GTT GCT TTA TTA GTA GAT GGT TTA CCT CAA ACG CAA TCT
Arg Asn Arg Val Ala Ile Val Asp Gly Leu Pro Gln Thr Gln Ser
290 295 300

TAT GTG CAA AGC CCT TTA GTT CCT CGT CGT TCA CGA TAT TCT CGC ACT
Tyr Val Val Gln Ser Pro Leu Val Ala Arg Ser Gly Tyr Ser Gly Thr
305 310 315

GGT GCA ATT AAT GAA ATT GAA TAT GAA AAT GAA AAG GCC GTC GAA ATA
Gly Ala Ile Asn Glu Ile Glu Tyr Glu Asn Val Lys Ala Val Glu Ile
320 325 330

AGC AAG GGG GCG AGT TCT TCT GAG TAT CGT AAT GCA GCA CTA CCT CGT
Ser Lys Gly Gly Ser Ser Glu Tyr Gly Asn Gly Ala Leu Ala Gly
335 340 345

FIG. 76.

TCT GTA ACA TTT CAA AGC AAA TCC GCA GCC GAT ATC TTA GAA GGA GAC

Ser Val Thr Phe Gln Ser Lys Ser Ala Ala Asp Ile Leu Glu Gly Asp
350 355 360 365

AAA TCA TGG CGA ATT CAA ACT AAA AAT GCT TAT TCA AGC AAA AAT AAA
Lys Ser Trp Gly Ile Gln Thr Lys Asn Ala Tyr Ser Ser Lys Asn Lys
370 375 380

GGC TTT ACC CAT TCT TTA GCT GTA CGA CGA AAA CAA CGT CGA TTT GAA
Gly Phe Thr His Ser Leu Ala Val Ala Gly Lys Gln Gly Gly Phe Glu
385 390 395

GGG GTC GCC ATT TAC ACT CAA CGA AAT TCG GAG GAA ACC CAA GTC CAT
Gly Val Ala Ile Tyr Thr Gln Arg Asn Ser Glu Glu Thr Gln Val His
400 405 410

AAA GAT GCA TTA AAA GGC GTA CAA AGT TAT GAG CGA TTC ATC GCC ACA
Lys Asp Ala Leu Lys Gly Val Gln Ser Tyr Glu Arg Phe Ile Ala Thr
415 420 425

ACA GAT AAA TCT TCA CGA TAC TTT GTG ATA CAA GGT GAG TGT CCA AAT
Thr Asp Lys Ser Ser Gly Tyr Phe Val Ile Gln Gly Glu Cys Pro Asn
430 435 440 445

FIG. 7 H.

CGT GAT GAC AAG TGT GCA GCC AAA CCA CCT GCA AAG TTA TCC CCC CAA
Gly Asp Asp Lys Cys Ala Ala Lys Pro Pro Ala Lys Leu Ser Pro Gln
450 455 460

AGC GAA ACC GTC AGC GTT TCA GAT TAT ACG GGG CCT AAC CGT ATC AAA
Ser Glu Thr Val Ser Val Ser Asp Tyr Thr Gly Ala Asn Arg Ile Lys
465 470 475

CCT AAT CCA ATG AAA TAT GAA AGC CAG TCT TCG TTT TTA AGA GGA CGG
Pro Asn Pro Met Lys Tyr Glu Ser Gln Ser Trip Phe Leu Arg Gly Gly
480 485 490

TAT CAT TTT TCT GAA CAA CAC TAT ATT GGT ATT TTT GAA TTC ACA
Tyr His Phe Ser Glu Gln His Tyr Ile Gly Gly Ile Phe Glu Phe Thr
495 500 505

CAA CAA AAA TTT GAT ATC CGT GAT ATG ACA TTT CCC GCT TAT TTA AGA
Gln Gln Lys Phe Asp Ile Arg Asp Met Thr Phe Pro Ala Tyr Leu Arg
510 515 520 525

TCA ACA GAA AAA CGG GAT GAT AGA ACT GGC CCT TTT TAT CCA AAG CAA
Ser Thr Glu Lys Arg Asp Asp Arg Thr Gly Pro Phe Tyr Pro Lys Gln
530 535 540

FIG. 71.

GAT TAT GGT GCA TAT CAA CGT ATT GAG GAT GGC CGA GGC GTT AAC TAT
Asp Tyr Gly Ala Tyr Gln Arg Ile Glu Asp Gly Arg Gly Val Asn Tyr
545 550 555

GCA AGT GGG CTT TAT TTC GAT GAA CAC CAT AGA AAA CAG CGT GTT GGT
Ala Ser Gly Leu Tyr Phe Asp Glu His His Arg Lys Gln Arg Val Gly
560 565 570

ATT GAA TAT ATT TAC GAA AAT AAG AAC AAA GCG GGC ATC ATT GAC AAA
Ile Glu Tyr Ile Tyr Glu Asn Lys Asn Ala Gly Ile Ile Asp Lys
575 580 585

GCA GTG TTA AGT GCT AAT CAA CAA AAC ATC ATA CTT GAC AGT TAT ATG
Ala Val Leu Ser Ala Asn Gln Gln Asn Ile Ile Leu Asp Ser Tyr Met
590 595 600

CCG CAT ACG CAT TGC AGT CCT TAT CCT AAT CCA AGT AAG AAT TGC CGC
Arg His Thr His Cys Ser Leu Tyr Pro Asn Pro Ser Lys Asn Cys Arg
610 615 620

CCG ACA CTT GAT AAA CCT TAT TCA TAC TAT CGT TCT GAT AGA AAT GTT
Pro Thr Leu Asp Lys Pro Tyr Ser Tyr Tyr Arg Ser Asp Arg Asn Val
630 635

FIG. 7 J.

TAT AAA GAA AAA CAT ATT ATG TTG CAA TTG AAT TTA GAG AAA AAA ATT
Tyr Lys Glu Lys His Asn Met Leu Gln Leu Asn Leu Glu Lys Lys Ile
640 645 650

CAA CAA AAT TCG CTT ACT CAT CAA ATT GTC TTC AAT CTT CGT TTT GAT
Gln Gln Asn Trp Leu Thr His Gln Ile Val Phe Asn Leu Gly Phe Asp
655 660 665

GAC TTT ACT TCA GCG CTT CAG CAT AAA GAT TAT TTA ACT CGA CGT GTT
Asp Phe Thr Ser Ala Leu Gln His Lys Asp Tyr Leu Thr Arg Arg Val
670 675 680 685

ACC GCT ACG GCA AAT ATT ATT TCA GGG ACA GTT GCT AAA CGA CGA
Thr Ala Thr Ala Asn Ile Ile Ser Gly Thr Val Ala Gly Lys Arg Arg
690 695 700

AAT GGT TAC GAA AAA CAA CCT TAC TTA TAC TCA AAA CCA AAA GTA GAT
Asn Gly Tyr Glu Lys Gln Pro Tyr Leu Tyr Ser Lys Pro Lys Val Asp
705 710 715

TTT GTA GGA CAA GAT CAT TGT AAT TAT AAA GGT AGC TCC TCT AAT TAC
Phe Val Gly Gln Asp His Cys Asn Tyr Lys Gly Ser Ser Ser Asn Tyr
720 725 730

FIG. 7K.

AGC GAC TGT AAA GTG CGG TTA ATT AAA GGG AAA AAT TAT TAT TTC GCA
Ser Asp Cys Lys Val Arg Leu Ile Lys Gly Lys Asn Tyr Tyr Phe Ala
735 740 745

GCA CGC AAT AAT ATG GCA TTA CGG AAA TAC ATT GAT TTA GGT TTA GGT
Ala Arg Asn Asn Met Ala Leu Gly Lys Tyr Ile Asp Leu Gly Leu Gly
750 755 760 765

ATT CGG TAT GAC GTC TCT CGT ACA AAA GCT AAT GAA TCA ACT ATT AGT
Ile Arg Tyr Asp Val Ser Arg Thr Lys Ala Asn Glu Ser Thr Ile Ser
770 775 780 785

GTT CGT AAA TTT AAA AAT TTC TCT TCT TCG AAT ACT GGT ATT GTC ATA AAA
Val Gly Lys Phe Lys Asn Phe Ser Thr Asn Thr Gly Ile Val Ile Lys
790 795

CCA ACG GAA TCG CTT GAT CTT TCT TAT CGC CTT TCT ACT GGA TTT AGA
Pro Thr Glu Trp Leu Asp Leu Ser Tyr Arg Leu Ser Thr Gly Phe Arg
800 805 810 815

AAT CCT AGT TTT CCT GCA ATG TAT GGT TGG CGG TAT GGT GGC AAT AAT
Asn Pro Ser Phe Ala Glu Met Tyr Gly Trp Arg Tyr Gly Gly Asn Asn
820 825

F16.7L.

AGC GAT GTT TAT GTA GGT AAA TTT AAG CCT GAA ACA TCT CGT AAC CAA
Ser Asp Val Tyr Val Gly Lys Phe Lys Pro Glu Thr Ser Arg Asn Gln
835 840 845

GAG TTT GGT CTC GCT CTA AAA GGG GAT TTT GGT AAT ATT GAG ATC AGT
Glu Phe Gly Leu Ala Leu Lys Gly Asp Phe Gly Asn Ile Glu Ile Ser
850 855 860

CAT TTT AGT AAT GCT TAT CGA AAT CTT ATC GCC TTT GCT GAA GAA CTT
His Phe Ser Asn Ala Tyr Arg Asn Leu Ile Ala Phe Ala Glu Glu Leu
865 870 875

AGT AAA AAT GGA ACT ACT CGA AAG GGC AAT TAT GGA TAT CAT AAT GCA
Ser Lys Asn Gly Thr Thr Gly Lys Gly Asn Tyr Gly Tyr His Asn Ala
880 885 890

CAA AAT GCA AAA TTA GTT GGC GTA AAT ATA ACT GCG CAA TTA GAT TTT
Gln Asn Ala Lys Leu Val Gly Val Asn Ile Thr Ala Gln Leu Asp Phe
895 900 905

AAT GGT TTA TGG AAA CGT ATT CCC TAC CGT TCG TAT GCA ACA TTT GCT
Asn Gly Leu Trp Lys Arg Ile Pro Tyr Gly Trp Tyr Ala Thr Phe Ala
910 915 920 925

FIG. 7M.

TAT AAC CGA GTA AAA GTT AAA GAT CAA AAA ATC AAT GCT GGT TTG GCC
Tyr Asn Arg Val Lys Val Lys Asp Gln Lys Ile Asn Ala Gly Leu Ala
930 935 940

TCC GTA AGC AGT TAT TTA TTT GAT CCC ATT CAG CCC AGC CGT TAT ATC
Ser Val Ser Ser Tyr Leu Phe Asp Ala Ile Gln Pro Ser Arg Tyr Ile
945 950 955

ATT GGT TTA GGC TAT GAT CAT CCA AGT AAT ACT TGG GGA ATT AAT ACA
Ile Gly Leu Gly Tyr Asp His Pro Ser Asn Thr Thr Gly Ile Asn Thr
960 965 970

ATG TTT ACT CAA TCA AAA GCA AAA TCT CAA AAT GAA TTG CTA GGA CAA
Met Phe Thr Gln Ser Lys Ala Lys Ser Gln Asn Glu Leu Gly Gln
975 980 985

CGT GCA TTG CGT AAC AAT TCA AGG AAT GTA AAA TCA ACA AGA AAA CTT
Arg Ala Leu Gly Asn Ser Arg Asn Val Lys Ser Thr Arg Lys Leu
990 995 1000

ACT CGG GCA TGG CAT ATC TTA GAT GTC TCG GGT TAT TAC ATG GCG AAT
Thr Arg Ala Thr His Ile Leu Asp Val Ser Gly Tyr Tyr Met Ala Asn
1010 1015 1020

FIG. 7 N.

AAA AAT ATT ATG CTT CGA TTA GGG ATA TAT AAT TTA TTC AAC TAT CGC
Lys Asn Ile Met Leu Arg Leu Gly Ile Tyr Asn Leu Phe Asn Tyr Arg
1025 1030 1035

TAT GTT ACT TCG GAA CGG GTG CGT CAA ACA GCA CAA CGT GCG GTC ATT
Tyr Val Thr Thr Glu Ala Val Arg Gln Thr Ala Gln Gly Ala Val Asn
1040 1045 1050

CAA CAT CAA AAT GTT GGT AGC TAT ACT CGC TAC GCA GCA TCA GGA CGA
Gln His Gln Asn Val Gly Ser Tyr Thr Arg Tyr Ala Ala Ser Gly Arg
1055 1060 1065

AAC TAT ACC TTA ACA TTA GAA ATG AAA TTC TAAATTTAA TGCGCCAGAT
Asn Tyr Thr Leu Thr Leu Glu Met Lys Phe
1070 1075

GGCACTAGATA TGGTATATCT ATACCTTACT GGGGCATCTT TTTCGTCTT ATAATCTGCT
TAAGTAAAA ACCAAACTTC GATTTCAC AAGATCTTT CACGCATTAA TGTAAAATC
TCCGACAAATT TTACCGCAC TTTCCTCTAT TACAAAAACA ATAAGGATCC TTTCGTGACT
CTCTCAATCT TTGGAAGTT GCTGTACAA CTTCAGATCA AGTTTCAGGCC AGGGATCTTA
GGCACTTGGG TTCCGCC

FIG. 8 A.

AT ATG AAA TCT GTC CCT CTT ATC TCT GGT GCA CTT TCC TTT TTA TTA
Met Lys Ser Val Pro Leu Ile Ser Gly Gly Leu Ser Phe Leu Ile
1 5 10 15

AGT GCT TGT AGC GGG GCA GGT TCT TCT GAT GTC GAT GAC GTC TCT
Ser Ala Cys Ser Gly Gly Gly Ser Phe Asp Val Asp Val Ser
20 25 30

AAT CCC TCC TCT TCA AAA CCA CGT TAT CAA GAC GAT ACT TCA AGT TCA
Asn Pro Ser Ser Lys Pro Arg Tyr Gln Asp Asp Thr Ser Ser Ser
35 40 45

AGA ACA AAA TCT AAA TTG GAA AAT TTG TCC ATT CCT CCT TTA GGG GGA
Arg Thr Lys Ser Lys Leu Glu Asn Leu Ser Ile Pro Ser Leu Gly Gly
50 55 60

GGG ATG AAG TTA GTG GCT CAG AAT CCT CGT GAT AGG ACA AAA CCT AGT
Gly Met Lys Leu Val Ala Gln Asn Leu Arg Asp Arg Thr Lys Pro Ser
65 70 75

CTC TTA AAT GAA GAT GAC TAT ATG ATA TTT TCC TCA CCT TCA ACG ATT
Leu Leu Asn Glu Asp Asp Tyr Met Ile Phe Ser Ser Leu Ser Thr Ile
80 85 90 95

FIG. 8B.

AAA GCT GAT GTT GAA AAA GAA AAT AAA CAC TAT ACA AGT CCA GTT GGC
Lys Ala Asp Val Glu Lys Glu Asn Lys His Tyr Thr Ser Pro Val Gly
100 105 110

TCA ATA GAC GAG CCT AGT ACA ACA AAT CCA AAA GAA AAT GAT CAT CGA
Ser Ile Asp Glu Pro Ser Thr Thr Asn Pro Lys Glu Asn Asp His Gly
115 120 125

CAA AGA TAT GIA TAT TCA CGA CTT TAT TAT ATT CCA TCG TGG AAT TTA
Gln Arg Tyr Val Tyr Ser Gly Leu Tyr Tyr Ile Pro Ser Trp Asn Leu
130 135 140

AAC GAT CTT AAA AAT AAC AAG TAT TAT TAT TCT GGT TAC TAT CGA TAT
Asn Asp Leu Lys Asn Asn Lys Tyr Tyr Ser Gly Tyr Ile Pro Ser Trp Asn Leu
145 150 155

CGG TAT TAC TTT GGC AAG CAA ACA CCC ACT ACA TTA CCT GTA AAT GGC
Ala Tyr Tyr Phe Gly Lys Glu Thr Ala Thr Thr Leu Pro Val Asn Gly
160 165 170 175

AAA GTA ACG TAT AAA GGA ACT TGG AGC TTC ATC ACC GCA GCT GAA AAT
Lys Val Thr Tyr Lys Gly Thr Trp Ser Phe Ile Thr Ala Ala Glu Asn
180 185 190

FIG. 8C.

GGC AAA AGG TAT CCT TTG TTA AGT AAT GGC AGT CAA GCT TAT TTT CGA
Gly Lys Arg Tyr Pro Leu Leu Ser Asn Gly Ser Gln Ala Tyr Phe Arg
195 200 205

CGT AGT GCA ATT CCA GAA GAT ATT GAT TTA GAA GTT AAA AAT GAT GAG
Arg Ser Ala Ile Pro Glu Asp Ile Asp Leu Glu Val Lys Asn Asp Glu
210 215 220

AAT AGA GAA AAA GGG CTA GTG AGT GAA TTT AGT GCA GAT TTT GGG ACT
Asn Arg Glu Lys Gly Leu Val Ser Glu Phe Ser Ala Asp Phe Gly Thr
225 230 235

AAA AAA CTG ACA CGA CGA CTG TTT TAC ACC AAA AGA CAA ACT CAT ATT
Lys Lys Leu Thr Gly Gly Leu Phe Tyr Thr Lys Arg Gln Thr His Ile
240 245 250

CAA AAC CAT GAA AAG AAA AAA CTC TAT GAT ATA GAT GCC CAT ATT TAT
Gln Asn His Glu Lys Lys Leu Tyr Asp Ile Asp Ala His Ile Tyr
260 265 270

AGT AAT AGA TTC AGA GGT AAA GTA AAT CCT ACC CAA AAA GAT TCT AAA
Ser Asn Arg Phe Arg Gly Lys Val Asn Pro Thr Gln Lys Asp Ser Lys
275 280 285

F16.8D.

GAA CAT CCC TTT ACC AGC GAG GGA ACA TTA GAA GGT GGT TTT TAC CGG
Glu His Pro Phe Thr Ser Glu Gly Thr Leu Glu Gly Gly Phe Tyr Gly
295 300

CCT GAA CGT CAA GAA TTA CGA CGA AAG TTT TTA GCT GGC GAC AAA AAA
Pro Glu Gly Glu Leu Gly Lys Phe Leu Ala Gly Asp Lys Lys
305 310

GTT TTT GGG GTA TTT AGT GCC AAA GGA ACG GAA AAC AAA AAA TTA
Val Phe Val Phe Ser Ala Lys Gly Thr Glu Glu Asn Lys Lys Leu
320 325

CCC AAA GAA ACC TTA ATT GAT GGC AAG CTA ACT ACT TTC TCT ACT AAA
Pro Lys Glu Thr Leu Ile Asp Gly Lys Leu Thr Thr Phe Ser Thr Lys
340 345

ACA ACC GAT GCA AAA ACC AAT GCA ACA GCC AAT GCA ACA ACC AGT ACC
Thr Thr Asp Ala Lys Thr Asn Ala Thr Ala Asn Ala Thr Thr Ser Thr
355 360

GCA GCC AAT ACA ACA ACC GAT ACA ACA GCC AAT ACA ATA ACC GAT GCA
Ala Ala Asn Thr Thr Asp Thr Ala Asn Thr Ile Thr Asp Ala
370 375

FIG. 8E.

GAA AAC TTT AAG ACG AAA GAT ATA TCA AGT TTT GGT GAA CCT GAT TAC
Glu Asn Phe Lys Thr Lys Asp Ile Ser Ser Phe Gly Glu Ala Asp Tyr
385 390 395

CTT TTA ATT GAT AAT TAC CCT GTT CCT CTT TTA CCT GAG AGT GGT GAT
Leu Leu Ile Asp Asn Tyr Pro Val Pro Leu Leu Pro Glu Ser Gly Asp
400 405 410 415

TTC ATA AGT AAG CAC CAT ACT GTC GGA AAG AAA ACC TAT CAA GTC
Phe Ile Ser Ser Lys His His Thr Val Gly Lys Lys Thr Tyr Gln Val
420 425 430 435

AAA GCA TGT TGC AGT AAT CTA AGC TAT GTG AAA TTT GGT ATG TAT TAT
Lys Ala Cys Cys Ser Asn Leu Ser Tyr Val Lys Phe Gly Met Tyr Tyr
440 445 450 455

GAA GTC CCA CCT AAA GAA GAA GAC AAA GAA AAA GAA GAA AAA
Glu Val Pro Pro Lys Glu Glu Glu Lys Asp Lys Glu Lys Lys Glu Lys
450 455 460 465

GAA AAA GAA AAA CAA CGG ACA AAT CTA TCG AAC ACT TAT TAT CAA TTC
Glu Lys Glu Lys Gln Ala Thr Asn Leu Ser Asn Thr Tyr Tyr Gln Phe
465 470 475

FIG. 8F.

TTA TTA GGT CTC CGT ACT CCC AGT TCT GAA ATT CCT AAA CGA CGA CGT
Leu Leu Gly Leu Arg Thr Pro Ser Ser Glu Ile Pro Lys Gly Gly Ser
480 485 490 495

GCA AAA TAT CTC CGT AGT TGG TTT GGT TAT CTG AGC GAT GGT TCA ACA
Ala Lys Tyr Leu Gly Ser Thr Phe Gly Tyr Leu Ser Asp Gly Ser Thr
500 505 510

TCT TAC TCC CCC AGT GGT GAT AAG AAA CGC GAG AAC AAT GCT CTC GCC
Ser Tyr Ser Pro Ser Gly Asp Lys Lys Arg Glu Asn Asn Ala Leu Ala
515 520 525

GAG TTT AAT GTA AAT TTT GTC GAT AAA ACA TTA AAA CGC CAA TTA ATA
Glu Phe Asn Val Asn Phe Val Asp Lys Thr Leu Lys Gly Gln Leu Ile
530 535 540 545

CGA CAC GAT AAT CAA AAT ACC GTT TTT ACA ATT GAT GCA ACC TTT AAA
Arg His Asp Asn Gln Asn Thr Val Phe Thr Ile Asp Ala Thr Phe Lys
550 555

CGT CGT AAG AAC TTC ACT CGT ACA GCA ACC GCA AAC AAT GTA CGG
Gly Gly Lys Asn Asn Phe Thr Gly Thr Ala Thr Ala Asn Asn Val Ala
560 565 570 575

FIG. 8 G.

ATT GAT CCC CAA AGT ACA CAA GGC ACA TCT AAC GTC AAT TTC ACG GCA
Ile Asp Pro Gln Ser Thr Gln Gly Thr Ser Asn Val Asn Phe Thr Ala
580 585 590

ACA GTA MAT GGC GCA TTT TAT GGG CCG AAC GCT ACA GAA TTA GGC GGT
Thr Val Asn Gly Ala Phe Tyr Gly Pro Asn Ala Thr Glu Leu Gly Gly
595 600 605

TAT TTC ACC TAT AAC GGA AAT CCT ACA GAT AAA AGT TCC TCA ACC GTA
Tyr Phe Thr Tyr Asn Gly Asn Pro Thr Asp Lys Ser Ser Thr Val
610 615 620

CCT TCA TCA TCC AAT TCA AAA AAT GCA AGA GCT GCA GTT GTC TTT GGT
Pro Ser Ser Ser Lys Asn Ala Arg Ala Val Phe Gly
625 630 635

GCG AGA CAA CAA GIA GAA ACA ACC AAA TAATGGATA CTAAAATGA
Ala Arg Gln Gln Val Glu Thr Thr Lys
640 645

CTAAAAAAGC TTCTAGAAGC CGAATTG

FIG. 9 A.

GAATTCCAT TGGATCCAT ATG AAA TCT GTA CCT CCT ATC TCT CGT GGA CTT
Met Lys Ser Val Pro Leu Ile Ser Gly Gly Leu
1 5 10

TCC TTT TTA CTA AGT GCT TGT AGC GGA GGG GGG TCT TTT GAT GTA GAT
Ser Phe Leu Leu Ser Ala Cys Ser Gly Gly Ser Phe Asp Val Asp
15 20 25

AAC GTC TCT AAT CCA TCC TCT TCT AAA CCA CGT TAT CAA GAC GAT ACT
Asn Val Ser Asn Pro Ser Ser Ser Lys Pro Arg Tyr Gln Asp Asp Thr
30 35 40

TCA AGT TCA AGA ACA AAA TCT AAT TTG AAA AAG TTG TCC ATT CCT TCT
Ser Ser Ser Arg Thr Lys Ser Asn Leu Lys Leu Ser Ile Pro Ser
45 50 55

TTA GGG GGA GGG ATG AAG TTA GTG GCT CAG AAT CTT AGT GAT AAG AAC
Leu Gly Gly Met Lys Leu Val Ala Gln Asn Leu Ser Asp Lys Asn
60 65 70 75

AAA CCT AGT CTC TTA AAT GAA GAT GAC TAT ATA TCA TAT TTT TCC TCA
Lys Pro Ser Leu Leu Asn Glu Asp Asp Tyr Ile Ser Tyr Phe Ser Ser
80 85 90

FIG. 9B.

CTT TCT ACA ATT CAA GAT GAT GTT AAA AAA GAA AAT AAA GCA CGC CAT ACA
Leu Ser Thr Ile Gln Asp Val Lys Lys Glu Asn Lys Arg His Thr
95 100 105

AAT CCA GTT GGC TCA ATA GAC GAG CCT AAC GCA ACA AAT CCA CCC GAA
Asn Pro Val Gly Ser Ile Asp Glu Pro Asn Ala Thr Asn Pro Pro Glu
110 115 120

AAG CAT CAT GGA CAA AGA TAT GTA TAT TCA GGG CTT TAT TAT CCA
Lys His His Gly Gln Arg Tyr Val Tyr Ser Gly Leu Tyr Tyr Ile Pro
125 130 135

TCG TGG AGT CAT TCC TCA AAT GGC AAG CTT TAT TTA GGT TAC TAT CGA
Ser Trp Ser His Ser Asn Gly Lys Leu Tyr Leu Gly Tyr Tyr Gly
140 145 150 155

TAT GCG TTT TAT TAT GGT AAT AAA ACT GCA ACA AAC TTC CCA GTC AGC
Tyr Ala Phe Tyr Tyr Gly Asn Lys Thr Ala Thr Asn Leu Pro Val Ser
160 165 170

GGC ATA GCT AAA TAC AAA GGA ACT TGG GAT TTT ATT ACT GCA ACT AAA
Gly Ile Ala Lys Tyr Lys Gly Thr Trp Asp Phe Ile Thr Ala Thr Lys
175 180 185

FIG. 9C.

AAT GCC CAA CGT TAT TCT TTA TTT CGT AGC GCT TTT GGA GCT TAT AAT
Asn Gly Gln Arg Tyr Ser Leu Phe Gly Ser Ala Phe Gly Ala Tyr Asn
190 195 200

AGA CGC ACT GCT ATT TCA GAA GAT ATA GAT AAT TTA GAA AAT AAT CTA
Arg Arg Ser Ala Ile Ser Glu Asp Ile Asp Asn Leu Glu Asn Asn Leu
205 210 215

AAG AAT GGT GCG GGA TTA ACT AGT GAA TTT ACT GTC AAT TTT GGT ACG
Lys Asn Gly Ala Gly Leu Thr Ser Glu Phe Thr Val Asn Phe Gly Thr
220 225 230 235

AAA AAG CTC ACT CGA AAA CTT TAT TAT AAT GAA AGG GAA ACA AAT CTT
Lys Lys Leu Thr Gly Lys Leu Tyr Tyr Asn Glu Arg Glu Thr Asn Leu
240 245 250

AAT AAA TTA CAA AAG AGA AAA CAT GAA CTC TAT GAT ATA GAT GCC GAT
Asn Lys Leu Gln Lys Arg Lys His Glu Leu Tyr Asp Ile Asp Ala Asp
255 260 265

ATT TAT AGT AAT AGA TTC AGA CGT AAA GAA GTC AAG CCA ACA ACC CAA AAA
Ile Tyr Ser Asn Arg Phe Arg Gly Lys Val Lys Pro Thr Thr Gln Lys
270 275 280

FIG. 9D.

GAT TCT CAA GAA CAT CCC TTT ACC AGC GAG GGA ACA TTA GAA GGT GGT
Asp Ser Gln Glu His Pro Phe Thr Ser Glu Gly Thr Leu Glu Gly Gly
285 290 295

TTT TAT GGG CCT AAC GGT GAA GAA TTA GGA GGA AAG TTT TTA GCT GGC
Phe Tyr Gly Pro Asn Gly Glu Leu Gly Gly Lys Phe Leu Ala Gly
300 305 310 315

GAT AAC CGA GTT TTT GGG GTA TTT AGT GCC AAA GAA GAA GAA ACA AAA
Asp Asn Arg Val Phe Gly Val Phe Ser Ala Lys Glu Glu Thr Lys
320 325 330 335

GAC AAA AAA TTA TCC AGA GAA ACC TTA ATT GAT GGC AAG CTA ATT ACT
Asp Lys Leu Ser Arg Glu Thr Leu Ile Asp Gly Lys Leu Ile Thr
340 345

TTT AAA AGA ACT GAT GCA ACA ACC AAT ACA GCA CCC AAT GCA AAA ACC
Phe Lys Arg Thr Asp Ala Thr Thr Asn Thr Ala Ala Asn Ala Lys Thr
350 355 360

GAT GAA AAA AAC TTT ACG ACG AAA GAT ATA CCA AGT TTT GGT GAA GCT
Asp Glu Lys Asn Phe Thr Thr Lys Asp Ile Pro Ser Phe Gly Glu Ala
365 370 375

FIG. 9E.

GAT TAC CTT TTA ATT GAT AAT TAC CCT GTT CCT CCT TTC CCT TTC CCT GAA GAA
Asp Tyr Leu Leu Ile Asp Asn Tyr Pro Val Pro Val Pro Glu Pro Glu Glu
380 385 390 395

AAT ACT AAT GAT TTC ATA ACT AGT ACG CAC CAT AAC GTA GCA GAT AAA
Asn Thr Asn Asp Phe Ile Thr Ser Arg His His Lys Val Gly Asp Lys
400 405 410

ACC TAT AAA GTA GAA GCA TGT TGC AAG AAT CTA AGC TAT GTG AAA TTT
Thr Tyr Lys Val Glu Ala Cys Lys Asn Leu Ser Tyr Val Lys Phe
415 420 425

GGT ATG TAT TAT GAA GAC CCA TTA AAT GGA GAA AAT GGC AAA GAA GAA AAA
Gly Met Tyr Tyr Glu Asp Pro Leu Asn Gly Glu Asn Gly Lys Glu Lys
430 435 440 445

GAA AAA GAA AAA GAA AAA GAC AAA GAA CAA GCG ACA ACA TCT ATC
Glu Lys Glu Lys Asp Lys Glu Lys Gln Ala Thr Thr Ser Ile
450 455

AAG ACT TAT TAT CAA TTC TTA TTA GGT CAC CGT ACT GCC AAG GAC GAC
Lys Thr Tyr Tyr Gln Phe Leu Leu Gly His Arg Thr Ala Lys Ala Asp
460 465 470 475

FIG. 9F.

ATA CCT GCA ACG GGA AAC GTG AAA TAT CGC GGT AAT TGG TTT GGT TAT
Ile Pro Ala Thr Gly Asn Val Lys Tyr Arg Gly Asn Trp Phe Gly Tyr
480 485 490

ATT GGT GAT GAC AAG ACA TCT TAC TCC ACT ACT GGA GAT AAA AAT GCT
Ile Gly Asp Asp Lys Thr Ser Tyr Ser Thr Gly Asp Lys Asn Ala
495 500 505

GTC GCC GAG TTT GAT GTA AAT TTT GCC GAT AAA ACA TTA ACA GGC ACA
Val Ala Glu Phe Asp Val Asn Phe Ala Asp Lys Thr Leu Thr Gly Thr
510 515 520

TAA AAA CGA CAC GAT AAT GGA AAT CCC GTA TTT ACA ATT AAT GCA AGC
Leu Lys Arg His Asp Asn Gly Asn Pro Val Phe Thr Ile Asn Ala Ser
525 530 535

TTT CAA AGT GGT AAG AAT GAC TTC ACT GGT ACA GCA ACC GCA AAC AAT
Phe Gln Ser Gly Lys Asn Asp Phe Thr Gly Thr Ala Thr Ala Asn Asn
540 545 550 555

GTA GCG ATT GAT CCC CAA AAT ACA CAA ACC ACA TCT AGA GTC AAT TTC
Val Ala Ile Asp Pro Gln Asn Thr Gln Thr Thr Ser Arg Val Asn Phe
560 565 570

FIG. 9G.

ACG GCA ACA GTA AAC GGG GCA TTT TAT GGA CCT AAG GCT ACA GAA TTA
Thr Ala Thr Val Asn Gly Ala Phe Tyr Gly Pro Lys Ala Thr Glu Leu
575 580 585

GGC GGT TAT TTC ACT TAT AAC GGA AAC AAT CCT ACA GAT AAA AAT TCC
Gly Gly Tyr Phe Thr Tyr Asn Gly Asn Asn Pro Thr Asp Lys Asn Ser
590 595 600

TCA ACC GTT TCA CCA TCC AAT TCA GCA AAT GCT CGT GCT GCC GTT GTG
Ser Thr Val Ser Pro Ser Asn Ala Asn Ala Arg Ala Ala Val Val
605 610 615

TTT GGC GCT AAA AAA CAA GTA GAA ACA ACC AAC AAG TAAAGAAC
Phe Gly Ala Lys Lys Gln Val Glu Thr Thr Asn Lys
620 625 630

CAAGTAATGG AATACTAAA ATGACTAAA AAGCTTCTAG AAAGCCGAT TC

FIG.10A.

ATG AAA TCT GTA CCT CCT ATC TCT GGT CGA CCT TCC CTT TTA TTA AGT
Met Lys Ser Val Pro Leu Ile Ser Gly Gly Leu Ser Leu Leu Ser
1 5 10 15

CCT TGT AGC CGG CGA CGT CGT TCT TTT GAT GTA GAT GAC GTC TCT AAT
Ala Cys Ser Gly Gly Ser Phe Asp Val Asp Val Ser Asn
20 25 30

CCC TCC TCT TCT AAA CCA CGT TAT CAA GAC GAT ACC TCG AGT CAA AGA
Pro Ser Ser Lys Pro Arg Tyr Gln Asp Asp Thr Ser Ser Gln Arg
35 40 45

ACA AAA TCT AAT TTG GAA AAG TTG TCC ATT CCT TCT TTA CGA CGA CGG
Thr Lys Ser Asn Leu Glu Lys Leu Ser Ile Pro Ser Leu Gly Gly Gly
50 55 60

ATG AAA TTG GTG GCT CAG AAT CTG AGT GGT AAT AAA GAA CCT AGT TTC
Met Lys Leu Val Ala Gln Asn Leu Ser Gly Asn Lys Glu Pro Ser Phe
65 70 75 80

TTA AAT CGA AAT GAC TAT ATG ATA TTT TCC TCA CGT TCT ACG ATT AAA
Leu Asn Gly Asn Asp Tyr Met Ile Phe Ser Ser Arg Ser Thr Ile Lys
85 90 95

FIG. 10B.

GAT GAT GTT GAA AAT AAC AAT ACA AAC GCG GCG GAC TAT ATT GCC TCA
Asp Asp Val Glu Asn Asn Asn Thr Asn Gly Gly Asp Tyr Ile Gly Ser
100 105 110

ATA GAC GAG CCT ACT ACA ACA AAT CCA CTC GAA AAG CAT CAT GGA CAA
Ile Asp Glu Pro Ser Thr Thr Asn Pro Leu Glu Lys His His Gly Gln
115 120 125

ACG TAT GTA TAT TCA GGG CTT TAT TAT CAA TCG TCG AGT CTA AGA
Arg Tyr Val Tyr Ser Gly Leu Tyr Tyr Ile Gln Ser Thr Ser Leu Arg
130 135 140

GAT TTA CCA AAG AAG TTT TAT TCA CGT TAC TAT CGA TAT CGG TAT TAC
Asp Leu Pro Lys Phe Tyr Ser Gly Tyr Tyr Ala Tyr Tyr
145 150 155 160

TTT GGC AAG GAA ACA GCC ACT ACA TTA CCT GTC AAT GGC GAA GCA ACG
Phe Gly Lys Glu Thr Ala Thr Thr Leu Pro Val Asn Gly Glu Ala Thr
165 170 175

TAT AAA GGA ACT TCG GAT TTC ATC ACT GCA ACT AGA AAT GGC AAA AGT
Tyr Lys Gly Thr Thr Asp Phe Ile Thr Ala Thr Arg Asn Gly Lys Ser
180 185 190

FIG.10C.

TAT TCT TTG TTA AGT AAT AAC CGA CAA CCT TAT TCC AAA CGT AGT GCA
Tyr Ser Leu Leu Ser Asn Asn Arg Gln Ala Tyr Ser Lys Arg Ser Ala
195 200 205

ATT CCA GAA GAC ATT GAT TTA GAA MAT GAT CCA AAG AAT CGT GAG ACG
Ile Pro Glu Asp Ile Asp Leu Glu Asn Asp Pro Lys Asn Gly Glu Thr
210 215 220

AGA TTA ACT AGT GAA TTT ACT GTG AAT TTT CGT ACG AAA AAG CTC ACA
Arg Leu Thr Ser Glu Phe Thr Val Asn Phe Gly Thr Lys Lys Leu Thr
225 230 235 240

CGT CGA CTT TAT TAC CAT TTA CGT AAA ACA AAT GCT AAT GAA AAC CAA
Gly Gly Leu Tyr Tyr His Leu Arg Lys Thr Asn Ala Asn Glu Asn Gln
245 250 255

AAT AGA AAA CAT AAA CTC TAC AAT CTA GAA CCT GAT GTG TAT AGC AAC
Asn Arg Lys His Lys Leu Tyr Asn Leu Glu Ala Asp Val Tyr Ser Asn
260 265 270

CCG TTC AGA CGT AAA GTA AAG CCA ACC AAA GAG TCT TCT GAA GAA CAT
Arg Phe Arg Gly Lys Val Lys Pro Thr Lys Glu Ser Ser Glu Glu His
275 280 285

FIG. 10D.

CCC TTT ACC AGC GAG CGA ACA TTA GAA GGT TTT CCT TAT GGG CCT AAT
Pro Phe Thr Ser Glu Gly Thr Leu Glu Gly Phe Tyr Gly Pro Asn
290 295 300

GCT GAA GAA CTA CGG CGA AAA TTT TTA GCT AGC GAT AAA AAA GTT TTT
Ala Glu Glu Leu Gly Gly Lys Phe Leu Ala Ser Asp Lys Lys Val Phe
305 310 315 320

GGG GTA TTT AGT GCC AAA GAA CAG CAA GAA ACG GAA GAA AAC AAA AAA
Gly Val Phe Ser Ala Lys Glu Gln Gln Glu Thr Glu Glu Asn Lys Lys
325 330 335 340

TTA CTC AAA GAA ACC TTA ATT GAT GGC AAG CTA ACT ACT TTC TCT ACT
Leu Leu Lys Glu Thr Leu Ile Asp Gly Lys Leu Thr Thr Phe Ser Thr
345 350 355 360

AAA AAA ACC AAT GCA ACA ACC GAT GCA ACA ACC AGT ACA ACA ACC AGT
Lys Lys Thr Asn Ala Thr Thr Asp Ala Thr Thr Ser Thr Thr Ser
355 360 365 370

ACA GCA ACC AAT GCA ACA GCC GAT GCA GAA AAC TTT ACG ACA AAA GAT
Thr Ala Thr Asn Ala Thr Ala Asp Ala Glu Asn Phe Thr Thr Lys Asp
370 375 380

F16.10E.

ATA TCA AGT TTT GGT GAA GCT GAT TAT CTT TTA ATT GAT AAT TAC CCT
Ile Ser Ser Phe Gly Glu Ala Asp Tyr Leu Ile Asp Asn Tyr Pro
385 390 395 400

GTT CCT CCT TTA CCT GAA AAT ACT AAT GAT TTC ATA ACC ACT AAT AAG CAC
Val Pro Leu Leu Pro Glu Asn Thr Asn Asp Phe Ile Ser Ser Lys His
405 410 415

CAT GAG GTA GCA GGT AAA CAC TAT AAA GTG GAA GCA TGT TGC AAG AAT
His Glu Val Gly Lys His Tyr Lys Val Glu Ala Cys Cys Lys Asn
420 425 430

CTA AGC TAT GTG AAA TTT GGT ATA TAT TAT GAG GAT AAT GAG AAG AAC
Leu Ser Tyr Val Lys Phe Gly Ile Tyr Tyr Glu Asp Asn Glu Lys Asn
435 440 445

ACC AAA ATT GAA ACA CAA TAC CAC CAA TTT TTG TTA GGT CTC CGT
Thr Lys Ile Glu Thr Glu Gln Tyr His Gln Phe Leu Leu Gly Leu Arg
450 455 460

ACT CCC AGT TCT CAA ATT CCT GCA ACG GCA AAC GTG AAA TAT CGC GGT
Thr Pro Ser Ser Gln Ile Pro Ala Thr Gly Asn Val Lys Tyr Arg Gly
465 470 475 480

F16.10F.

AGT TCG TTT GGT TAT ATT GGT GAT GAC AAG ACA TCT TAC TCC ACT ACT
Ser Trp Phe Gly Tyr Ile Gly Asp Asp Lys Thr Ser Tyr Ser Thr Thr
485 490 495

GGA GAT AAA AAT GCT CTC GCC GAG TTT GAT GTA AAT TTT ACC GAT AAA
Gly Asp Lys Asn Ala Leu Ala Glu Phe Asp Val Asn Phe Thr Asp Lys
500 505 510

AAG CTA ACA GGC GAA TTA AAA CGA CGA GAT AAT CAA AAT ACC GTA TTT
Lys Leu Thr Gly Glu Leu Lys Arg Ala Asp Asn Gln Asn Thr Val Phe
515 520 525

AGA ATT AAT GCA GAC TTT AAA AAT GAT AAT GCC TTC AAA GGT ACA
Arg Ile Asn Ala Asp Phe Lys Asn Asn Asp Asn Ala Phe Lys Gly Thr
530 535 540

GCA ACC GCA GAA AAT TTT GTA ATA GAT CGT AAC AAT AGT CAA ACT GGA
Ala Thr Ala Glu Asn Phe Val Ile Asp Gly Asn Asn Ser Gln Thr Gly
545 550 555

AAT ACC CAA ATT AAT ATT AAA ACT GAA GTA AAT GGG GCA TTT TAT GGT
Asn Thr Gln Ile Asn Ile Lys Thr Glu Val Asn Gly Ala Phe Tyr Gly
565 570 575

FIG. 10 G.

CCG AAC CCT ACA GAA TTA GGC GGT TAT TTC ACT TAT AAC GGA AAA AAT
Pro Asn Ala Thr Glu Leu Gly Tyr Phe Thr Asn Gly Lys Asn
580 585 590 595

CCT ACA GAT AAA AAT TCT GAA AGT TCC TCA ACC GTC CCT TCA CCA CCC
Pro Thr Asp Lys Asn Ser Glu Ser Ser Ser Thr Val Pro Ser Pro Pro
595 600 605

AAT TCA CCA AAT GCA AGA CCT GCA GTT GTC TTT GGT GCT AAA AAA CAA
Asn Ser Pro Asn Ala Arg Ala Ala Val Val Phe Gly Ala Lys Lys Gln
610 615 620

GTA GAA AAA AAC AAC AAG TAAACAAAC CAAGTAAATGG ATACTAAAA
Val Glu Lys Asn Asn Lys
625 630

ATGACTAAAA AAGCTCTAG AAGCCCCATT C

FIG. 11A.

ATG AAA TCT GTT CCT CTT ATC TCT CGT CGA CCT TCC TTT TTA CTA AGT
Met Lys Ser Val Pro Leu Ile Ser Gly Gly Leu Ser Phe Leu Leu Ser
1 5 10 15

GCT TGT AGC CGA CGG CGG TCT TTT GAT GTA GAT AAC GTC TCT AAT ACC
Ala Cys Ser Gly Gly Ser Phe Asp Val Asp Asn Val Ser Asn Thr
20 25 30

CCC TCT TCT AAA CCA CGT TAT CAA GAC GAT ACC TCG AAT CAA AGA ACA
Pro Ser Ser Lys Pro Arg Tyr Gln Asp Asp Thr Ser Asn Gln Arg Thr
35 40 45
AAA TCT AAA TTG GAA AAG TTG TCC ATT CCT TCT TTA GGA CGA CGG ATG
Lys Ser Lys Leu Glu Lys Leu Ser Ile Pro Ser Leu Gly Gly Gly Met
50 55 60

AAG TTA GTT GTG CAA AAT TTT CCT CGT GCT AAA GAA CCT AGT TTC TTA
Lys Leu Val Val Gln Asn Phe Ala Gly Ala Lys Glu Pro Ser Phe Leu
65 70 75 80

AAT GAA AAT GAC TAT ATA TCA TAT TTT TCC TCA CCT TCT ATG ATT AAA
Asn Glu Asn Asp Tyr Ile Ser Tyr Phe Ser Ser Leu Ser Met Ile Lys
85 90 95

F16.11B.

GAT GAT GTT GAA AAT AAC AAT AAA AAT AAG GAT ACT CCA ATT GGC TCA
Asp Asp Val Glu Asn Asn Lys Asn Lys Asp Thr Pro Ile Gly Ser
100 105 110

ATA GAC GAG CCT AGA GCA CCA AAT TCA AAC GAA AAT CAT CAA AAT CAT
Ile Asp Glu Pro Arg Ala Pro Asn Ser Asn Glu Asn His Gln Asn His
115 120 125

CAT GGA CAG CAA TAT GTA TAT TCG CGT CTT TAT TAT CCA TCG TGG
His Gly Gln Gln Tyr Val Tyr Ser Gly Leu Tyr Tyr Ile Pro Ser Thr
130 135 140

CGT CTA ATA AAT TTA CCA AAT AAG TTT TAT TCA CGT TAC TAT GGA TAT
Arg Leu Ile Asn Leu Pro Asn Lys Phe Tyr Ser Gly Tyr Tyr Gly Tyr
145 150 155 160

GGC TAT TAC TTT GGC AAG CAA ACT GCC ACT ACA TTA CCT GTA AAT GGC
Ala Tyr Tyr Phe Gly Lys Gln Thr Ala Thr Thr Leu Pro Val Asn Gly
165 170 175

GAA GCA ACG TAT AAA GGA ACT TGG ACC TTC ATC ACC GCA ACT GAA AGA
Glu Ala Thr Tyr Lys Gly Thr Trp Ser Phe Ile Thr Ala Thr Glu Arg
180 185 190

FIG.11C.

GGC AAA MAT TAT TCT TTG TTC AAT AAT AGA GGT CAA GCT TAT TCT CGA
Gly Lys Asn Tyr Ser Leu Phe Asn Asn Arg Gly Gln Ala Tyr Ser Arg
195 200 205

CGT AGT GCT ACT CCA CGA GAT ATT GAT TTA GAA AAC GGT GAC GCA GGC
Arg Ser Ala Thr Pro Gly Asp Ile Asp Leu Glu Asn Gly Asp Ala Gly
210 215 220

TAA ACA ACT GAA TTT ACT GTC AAT TTT CGT ACA AAA AAG CTC ACT CGA
Leu Thr Ser Glu Phe Thr Val Asn Phe Gly Thr Lys Lys Leu Thr Gly
225 230 235 240

GAA CCT TAT TAT GAA AGG GAA ACA AAT CTT AAT CAA TCA AAA GAT
Glu Pro Tyr Tyr Asn Glu Arg Glu Thr Asn Leu Asn Gln Ser Lys Asp
245 250 255

AGA AAA CAT AAA CTC TAC GAT CTA GAA GCT GAT GTG TAT AGC AAC CGA
Arg Lys His Lys Leu Tyr Asp Leu Glu Ala Asp Val Tyr Ser Asn Arg
260 265 270

TTC AGA GGT ACA GTA AAG CCA ACC AAA GAG TCT TCT GAA GAA CAT
Phe Arg Gly Thr Val Lys Pro Thr Lys Glu Ser Ser Glu Glu His
275 280 285

FIG. 11D.

CCC TTT ACC AGC GAG CGA ACA TTA GAA GGT GGT TTT TAT GGG CCT AAT
Pro Phe Thr Ser Glu Gly Thr Leu Glu Gly Gly Phe Tyr Gly Pro Asn
290 295 300

GCT GAA GAA CTA GGG CGA AAA TTT TTA GCT AGC GAT AAA AAA GTT TTT
Ala Glu Glu Leu Gly Gly Lys Phe Leu Ala Ser Asp Lys Lys Val Phe
310 315 320

GCG GTA TTT AGT GCC AAA GAA ACG GAA AAA CCA AAA TTA CCC AAA
Gly Val Phe Ser Ala Lys Glu Thr Glu Glu Lys Pro Lys Leu Pro Lys
325 330 335

GAA ACC TTA ATT GAT CGC AAG CTA ACT ACT TTC TCT AAA ACA ACC GAT
Glu Thr Leu Ile Asp Gly Lys Leu Thr Thr Phe Ser Lys Thr Thr Asp
340 345 350

ACA ACA ACC AAT AAA ACA ACC AGT GCA AAA ACC AAT ACA GAA AAC TTT
Thr Thr Asn Lys Thr Thr Ser Ala Lys Thr Asn Thr Glu Asn Phe
355 360 365

ACG ACA AAA GAT ATA CCA AGT TTT GGT GAA GCT GAT TAT CTT TTA ATT
Thr Thr Lys Asp Ile Pro Ser Phe Gly Glu Ala Asp Tyr Leu Leu Ile
370 375 380

FIG. 11E.

GAT AAT TAC CCT ATT CCG CTT TTA CCT GAG AGT GGT GAT TTC ATA AGT
Asp Asn Tyr Pro Ile Pro Leu Leu Pro Glu Ser Gly Asp Phe Ile Ser
385 390 395 400

AGT AAG CAC CAT GAG GAA CGT AAA CGC TAT AAA GTC GAA GCA TGT
Ser Lys His His Glu Val Gly Gly Lys Arg Tyr Lys Val Glu Ala Cys
405 410 415

TGC AAC AAT CTA TGC TAT GTG AAA TTT GGT ATG TAT GAG GAT AAA
Cys Lys Asn Leu Cys Tyr Val Lys Phe Gly Met Tyr Glu Asp Lys
420 425 430

GAG AAC AAC AAA AAT GAA ACA GAC AAA GAA AAA GAA CAA CAA ACG ACA
Glu Asn Asn Lys Asn Glu Thr Asp Lys Glu Lys Glu Lys Gln Thr Thr
435 440 445

ACA TCT ATC AAC ACT TAT TAT CAA TTC TTA TTA GGT CTC CGG ACT CCC
Thr Ser Ile Lys Thr Tyr Tyr Gln Phe Leu Leu Gly Leu Arg Thr Pro
450 455 460

AGT TCT GAA ATT CCT AAA ATG GGA AAC GTG ACA TAT CGC CGT AGT TCG
Ser Ser Glu Ile Pro Lys Met Gly Asn Val Thr Tyr Arg Gly Ser Thr
465 470 475 480

FIG. 11F.

TTT GGT TAT ATT GGT GAT GAC AAG ACA TCT TAC TCC GCT ACA CGA GAT
Phe Gly Tyr Ile Gly Asp Asp Lys Thr Ser Tyr Ser Ala Thr Gly Asp
485 490 495

AAA CGA CAA GAT AAA AAT GCT CCC GCC GAG TTT AAT GCT GAT TTT AAC
Lys Arg Gln Asp Lys Asn Ala Pro Ala Glu Phe Asn Ala Asp Phe Asn
500 505 510

AAT AAA AAG CTA ACA GGC ACA TCA AAA CGA CAC GAT AAT CAA AAT CCC
Asn Lys Lys Leu Thr Gly Thr Ser Lys Arg His Asp Asn Gln Asn Pro
515 520 525

GIG TTT AAC ATT AAG GCA ACC TTT CAA AAT GGT CGG AAT GAC TTT GAA
Val Phe Asn Ile Lys Ala Thr Phe Gln Asn Gly Arg Asn Asp Phe Glu
530 535 540

GGT ACA GCA ACC GCA GAA AAT TTT GTA ATA GAT CGT AAA GAT AGT CAA
Gly Thr Ala Thr Ala Glu Asn Phe Val Ile Asp Gly Lys Asp Ser Gln
545 550 555

CGA AAT ACC CCA ATT AAT ACA ACT AAA GTA AAC GGG GCA TTT TAT
Gly Asn Thr Pro Ile Asn Ile Thr Thr Lys Val Asn Gly Ala Phe Tyr
565 570 575

FIG. 116.

CGA CCT GAT GCT TCT GAA TTA GGC GGT TAT TTC ACC TAT AAC GGA AAA
Gly Pro Asp Ala Ser Glu Leu Gly GLY Tyr Phe Thr Tyr Asn Gly Lys
580 585 590

GAC ACT ATA ACT AAA AAT ACT GAA AGT TCC TCA ACC GTC CCT TCA CCA
Asp Thr Ile Thr Lys Asn Thr Glu Ser Ser Ser Thr Val Pro Ser Pro
595 600 605

CCC AAT TCA CCA AAT GCA AGA GCT GCA GTT GTC TTT GGA GCT AAA AAA
Pro Asn Ser Pro Asn Ala Arg Ala Val Val Phe Gly Ala Lys Lys
610 615 620 625

CAA GTA GAA ACA ACC AAC AAG TAGAAAAAA CAAATAATGG AATACTAAAAA
Gln Val Glu Thr Thr Asn Lys
625 630

ATGACTAAAA AAGCTCTAG AAAGCCGAAT TC

FIG. 12A

FIG. 12B

3' *tbp2*

5' *tbp1*

M T K K

GTAGAAACCAACCAATAA-----TGGAAATACTAAAAATGACTAAACCCCTATTTTGCCTAAGT EAGAN
GTAGAAACCAACCAATAA-----TGGAAATACTAAAAATGACTAAACCCCTATTTTGCCTAAGT MINNA
GTAGAAACCAACCAAGTAA-----TGGAAATACTAAAAATGACTAAACCCCTATTTTGCCTAAGT DL63

GTAGAAACCAACCAAGTAATGGAATACTAAAAATGACTAAACCCCTATTTTGCCTAAGT PAK

3' TACCTTAIGATTTTACIGATTTT \CGAAGATCT 5'

M T K K

GTAGAAACCAACCAATAA-----TGGAAATACTAAAAATGACTAAAAAA SB12

GTAGAAACCAACCAAGTAAACCAACCAAGTAATGGAATACTAAAAATGACTAAAAAA SB29

GTAGAAACCAACCAACTAGTAAACCAACCAAGTAATGGAATACTAAAAATGACTAAAAAA SB30

GTAGAAACCAACCAAGTAAACCAACCAAGTAATGGAATACTAAAAATGACTAAAAAA SB32

1 2 3 4 5

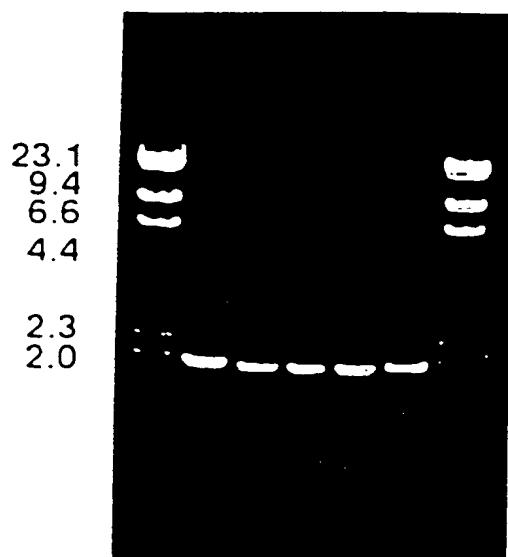


FIG.13.

FIG.14 A.

Comparison of TBPI amino acid sequences

MTKKPYFRLSIISCLLISCVKAETQSIIKDTKEAISSEVDTQSTEDSELETISVTAEKIRDKDNEVTGLGKIIKTTSESISREQVLNIRDTRYDPGISV	EAGAN
.....V.....	DL63
.....PAK.....	PAK
.....SB33.....	SB33
.....B16B.....	B16B
.....M982.....	M982
.....FA19.....	FA19
.....	
VEQGRGASSGYSIRGMDRNRVALLVDGLPQTQSYVVQSPPLVARSGYSGTGAINEIEYENVKAVEISKGGSSEYGNCALGSVTFQSksAADILEGDKSW	EAGAN
.....	DL63
.....PAK.....	PAK
.....SB33.....	SB33
.....B16B6.....	B16B6
.....M982.....	M982
.....FA19.....	FA19
.....	
GIOTKNAVSSKNNKGFTHSLAVAGKQGGFEGLAIYTORNSTETQVHDKALKGVQSYDRLLIATTDKSSSGYFV1QG-----ECPNGDDK--CAA--KPPATLS	EAGAN
.....V.....H.....	DL63
.....F.....EDQ.A...M.D-----LD.Y...KTSP.R.....	PAK
.....H.....KPEDQ.A...M.D-----KP.YNS.LPFA.R.I..	SB33
.....F.....	SB33
.....V.....E.....	B16B6
.....F.....	M982
.....V.....	FA19
.....	
S.T...G.DHAL.Q...L.RS.A.A.L..K.RGR.IHA...G.....FN..VLDE..KE.GSQYRYFIVEE..H..YAA--.KNKL.ED.SVK	
S.T...G.R.L.Q.I.L..RI.A.A.L.H.K.RGG.IRA.E..GR.....FN..VLVE..SSEYAYFIVED..EGKNYET..KSKP.KDVVGK	
S.T...G.R.L.Q.I.L..RI.A.A.L.H.K.RGG.IRA.EA.GR.....FN..APVD..GSKYAYFIVEE..K..GHEK-.K.NP.KDVVG	

FIG. 14B.

--GVKYASGLYFDEHHRKQRGIEYIYENKNKAGIIDKAVL SANQNIILD SYMRHTHCSLYPNPSKNCRPTLDKPSSYYRSDRNVYKEKHNMLQL
EAGAN
DL63
PAK
SB33
B16B6
M982
FA19

NYYFAARNNMALGKYVDLGLGIRYDVSRTKANESTISVGKFKNFSWNTGIVIKPTEWLDLSYRLSTGFRNPSFSEMYGWRYGGKNDEVYVGKFKPETSNN
EAGAN
DL63
PAK

FIG.14 C.

.....I.....A.....N.SD.....
 G..A.VQD.VR..RWA.V.A.....YRS.HSEDKSV.T.THR.L...A.V.L..FT.M..T..A.....L..A.....A.....A.--A.--ESLKTLDL...K.F.
 G..A.V.D.VR..RWA.V.A.L...YRS.HSSDDGSV.T.THRTL..A..L..AD...T..A.....L..A.....A.....S.--VQSKAV.ID..K.F.
 S..A.V.D.VR..RWA.V.A.L...YRS.HSSDDGSV.T.THRTL..A..L..AD...T..A.....L..A.....S.--.KIKAV.ID..K.F.
 FA19

QEFGLALKGDFGNIEISHFSNAYRNLLIAFAEELSKNG-TGKGNY--GYHNAQNAKLVGVNITAQLDNFGLWKRIPYGNYATFAYNQVKVKDQKINAGLAS
T.....-.....R.....
N..-..A..-.....R.....
T.....-.....R.....
 R.A.IVF.....L.A.Y.N...D...GY..TRTQNGQTSASGDP..R...RIA.I..LGKI.WH.V.GGL.D.L.S.L..RI...AD.R.DRTF
 K.A.IVF.....L.A.W.N...D..VRGY.AQIKNGKEEAKGDP.A.L...S.RIT.I..LGKI.W..V.DKL.E..S...R.H.R.I.KR.DRTD
 K.A.IVF.....L.A.W.N...D..VRGY.AQIKDGKEQVKGNPA.L...S.RIT.I..LGKI.W..V.DKL.E..S...R.R.R.I.KR.DRTD
 FA19

VSSYLFDAIQPSRYIIGLGYDHPSENWGINTMFTQSAKSQNELLGKRALGNNNSRD-VKSTRKLTRAWHILDVSGYMMANKNIMRLGIYNFLNYRYVTW
K.....N-.....V.RS.LF..V..L...
N-.....V.RS.LF..V..L...
Q.....N-.....V.RS.LF..V..L...
T.....V.....VL...DGI...Y.....VD...SQ..L.GNANAK.AASRR..P.YVT...NIK.HLT..A.V..L...
 IQ.H.....VV...Q.EGK..V.G.L.Y...EIT...S...L.GNSRNT.A.ARR..P.Y.V...TIK.HFT..A.V..L...
 IQ.H.....VV.S...Q.EGK..V.G.L.Y...EIT...S...L.GNSRNT.A.ARR..P.Y.V...TVK.HFT..A.V..L.H...
 FA19

EAVRQTAQGAVNQHQNVGSYTRYAASGRNYTLTLEMKF* EAGAN
* DL63
* PAK
* SB33
* B16B6
* M982
* FA19

SB33
 B16B6
 M982
 FA19

F16.15 A.

Comparison of TNP2 amino acid sequences

MKSVPLISGGLSFLLSACSGGG-SFVDVNTNSNTPS--SKPRYQDDTS---NQRKKS-NLKKLFIPSLLGGGMKLVAQNLRGNREPSFLNEDDYISYFSS	EAGAN
.....T.....G.....D.....PS.....	DL63
.....T.....G.....D.....PS.....	PAK
.....G.....D.....PS.....	SB12
.....G.....D.....PS.....	SB19
.....L.....G.....D.....PS.....	SB30
.....G.....D.....PS.....	SB32
.....G.....L.....S.....ETVODMH.....K.....E.....EK.....Q.....PES.....QDV.....E.....SGAAYGFAVKLPLRRNAHF.....PKYKFKHKP.....GSM.....WKKLO-R	B16B6
.....G.....L.....S.....DT-EAPRPA.....K.....VS.....EKPOA.....KD---QG-GYGFAMRLKRRRN--WYPGAAESEEVK...S.....WEATGLP	M982
.....G.....L.....S.....DT-EAPRPA.....K.....VP.....KKPEARKD---QG-GYGFAMRFYKRRRNQHPSANPKEDEVK.....KN.....WEATGLP	FA19
.....KG.....LED.....RPNKTTGVSKEEYK.....VETAKKEKEQ---GE.....ME.....A.....YV.....V.....VSSF.....MKKVDI---	AP205
.....KG.....LED.....RPNQATAEKATTSYQDEETKKKT.....EE.....D.....ME.....A.....YET---.I.....R.....A.....KTETGEKRNREV--	AP37
.....R.....E.....ND.....Q.....EHP.....D.....VD.....RAP.....SN.....R.....	EAGAN
.....E.....EKVKN.....GR.....E.....NG.....SQNSN.....S.....E.....	DL63
.....KA.....EK---E.....HYTSPV.....K.....N---D.....R.....	PAK
.....QD.....K---E.....RHTNPV.....NA.....	SB12
.....KD.....E---N.....T.....G.....Y.....L.....R.....	SB29
.....M.....KD.....E---N.....KDTP.....RAP.....SN.....NHQN.....Q.....	SB30
.....GEPNSFSERDE--L.....KRG-----SSE--E.....KW.....DG-----QSRVVGYTNTFT.....R.....YV.....LNK-NNI.....I.....NIV--LFGPDG.....Y.....KEPS	SB32
.....TKPKELPKRQK.....V.....VETDGDSDIYSSPY.....TR.....NHQNGSAGNGVN--QPKNQATGHENFQ.....WF.....KHA.....EK.....FS.....K.....I--KSGDDG.....IF.....H.....EKPS	B16B6
.....TEPKKLPLKQQ.....V.....SEVETNGNSKMYTSPY.....SQDA.....SSH--ANGAN--QPKNQEVTDYKKFK.....WF.....KHAK.....EVKNE.....GLVSAKRGDDG.....IF.....H.....DKPS	M982
.....D.....VITNGNL.....DVPYK.....NSSKKNYPDI.....KTKDSSLQ.....R.....YVIDGEH.....GSNE-----VY.....	FA19
.....AP205	AP37
.....VELSED.....IT.....LYQESVEIIPH.....DELNGKTTNSNDVYHS----DSKRLDKNRDLK.....R.....YV.....DG.....FNEIRRNDSG.....HVFKQGID-----VY.....	AP37

F16.15B.

YGNKTATNLPVNGVAKYKGTWDFITATKNGKRYPLLSNGS---HAYYRRSAIPPEDIDLENDSKNGDI-GLISEFSADFGTKKLTGQLSYTKRKT---N
 F..T..SA...G...T....S....AE...N.E..R.SGGG-Q...S....T....DRKT---T...TVN....G.Y.NL.E.DAN---K
 E..K....K....N....E....S.F..SIG--Q...S....S....YNLENGDA---V...K.E...E.Y.NE...SVN---E
 F.KQ..T...KVT...S...AE....Q...F....VKNDENREK..V....G.F...Q...H
 S.I....Q...S.FGSAF---G...N....S....NLENNKLNGA-..T...TVN....K.Y.NE.E...-N
 F.KE...T...E.T....R...S.S...NR--Q...SK....P...ETR--T...TVN....G.Y.HL...NAN---E
 F.KQ..T...E.T....S....ER..N.S.FN.RG---Q...S....T.G....A...T...TVN....EPY.NE.E.N---L
 KELP-SEKITYK.TWD.VTDAMEKQRFEGL--GSAAGGFYKSGALSALEEGVLRNQAEAS--SGHT.F--MT..EV..SD.TIK.T.YRNN.I.QNNSENKQ
 RQLPASGKVIYK..WHFVTDTKKGQDFREIIQPSKKQGDRYSGFSGDGSEEYSNKNNESTLKDHEGY-FT.NLEV...N...K.IRNNASILMNNTNNDK
 RQLPASEAVIYK..WHFVTDTKKGQKFNDILETSKGQGDYKSGFSGDDEGETSNRT.SNIND.HEGY-FT.N.KV..NN...K.IRNNKVINTAASDG-
 K..SP..KE...QLLT.T.S...TSMANLNNEEGRPNYLN---DD..TKFIGKRVGLVSG.A.PAKH-KYT.Q.EV..A..M..KJ..D.E...-
 L.VTPSKE..KGGK.IS....VSNINLEREIDGKDTSGDGKVNVSATSTITETVNR.HKVGE.L..N-EVKGVVAHSSEFAVDFDNKKLTGSLYRNGYINRK
 AP205
 AP37

EAGAN
 DL63
 PAK
 SB12
 SB29
 SB30
 SB32
 B16B6
 M982
 FA19
 AP205
 AP37

EAGAN
 DL63
 PAK
 SB12
 SB29
 SB30
 SB32
 B16B6
 M982
 FA19
 AP205
 AP37

NQ--PYEKKKLYDIDADIYSNRFRTVKPTEKD-SEEHPFTSEGT-LEGGFYGPNAEELGGKFLATNDRVFGVFSAKETEETKKEA-LSKETLIDGLITFFS
 S.--NRTH-...LE..VH....K...K..ES....-EGQ.....H..KK..L.....QQ..SENKK..P.....T..K
 S.--NTTH-...TLE..KV....K...KTK-..D....-N..EK.....DPQNPNQK..T.....K
 I.--NH....H....K.N..Q--K....-EGQ.....G..KK.....G..N...---P.....T...
 .NKLQKR.HE...K...TQKD.Q....-G.....G.....-DKK-..R.....K
 .--NR.H...NLE..V....K..KES-....S..KK.....QQ..EENKK..L.....T...
 .-SKDR.H...LE..V....K..ES-....S..KK.....KP...---P.....T...
 IK--TTRYTIQATHGNRFGKALAAD,GATNG-...I.DSDS....KG...A....SN..K.AA..G..QKDQKDG.NAAGPA.E---
 HT--TQYYSLDAQ.TGNRFGNTATA.D.KENET-KL--..V.DSSS.S...F..QG...FR..SD.QK.AV.G...TKDKLENG.AA.GS.GAAASGGAAG
 YT--TEYYSLDATLGNRFGKAIAD..NTGGTKL--..VFDSSS.S...F..QG...FR..SD.GK.AV.G...TKDSTANGNAPAAASSG---
 IY--TV---NA..RGNRFTGAATASD.NKG.GE.YNF-.SADSQS...K..MA...V.N.KSL.A...-
 A---.VT.R.S.E...AG...KA.A-..AGD---.IFTDSNY...K..MA...FTNNKSL.A..A...-
 AP205
 AP37

EAGAN
 DL63
 PAK
 SB12

TKKTDAKT---NATTSTAANTTDTANTITDEKNFKTEDISSFGEADYLLIDKY---PIPLLPDKNNDFFI
 .TNAT.NATT--D....T.S.K...T.ATANTE..T.K..P.L....N...-V..F--ESG...
 RTDATTNATT--D.K..ATTDA.S-..KK..AE...P...GNQ...E...D...
 .T...NATA...AE...K...N...-V...-ESG...
 EAGAN
 DL63
 PAK
 SB12

FIG.15C.

.....T.....A..AK.....T.K.....P.....N.....V.F.EE.....SB29
N.T.....D.....S.ATNATA,AE..T.K.....N.....V.....E.....SB30
KTD..NK.TSAK.NTE..T.K.P.....N.....V.....E.....ESG...SB32
VID.YRI.GEEFKKEQIDSFGDVKKLLVD.VELS..PSEGNAKA.....FOHEIE.....B16B6
SENS--KL..VLD.VEL.LNDKKIKNLDNFSNAAQLVVD..IMIP..PKDSESGNTQADKGKNGGTEFTRKFEHTPESDKKDAQAGTQNTGAGTASN.....M982
PGAATMPSET--RL..VLD.VEL.PDGKEIKNLDNFSNATRLVVD..IMIP..PT--ESGNGQADKGKNGGTDFTYETTYTPESDKKDTKAQTGAGGMOTASG.....FA19
HNGSNVN.VRIDASKI.LT..SISELNN..D.SV.I.....GKKIKLLAGSG.T.....AP205
SENG--ET..E--RIIDA.KI.LTQ.NAKELNN..D.SV.I.....GKKI.LAGVN.K.....AP37

SSKHHTVGNKR--YKVEACCSNLSYVFGMYYEDPLKEKETETEKDKEKEKDKDEKEQTAATNTYYQFLLGHTPKDDIPK--TGSAKYHGSWFG.....EAGAN
K.T--Q.....A.P.--E.K.K.KD.....ATTSIK.....L..SSE...--E.....N.....DL63
G.T--K.....KDKDN.NETDKEKGKEKPT.TTSI.....L.....E...--E.....N.....PAK
K.T--Q.K.....V.P..E.....KE.E...ATNLS.....L..SSE...--G.....L.....SB12
T.R..K..D.T--K.....NG.NG.....E.....ATTSIK.....A.A..A--..NV..R.N.....SB29
E..G.H--K.....I.....N..N.KIE.EQ.H.....L..SSQ..A--..NV..R.....SB30
E..G.--K..C.....I.....KENNKN.T..E.....TTSIK.....L..SSE...--M.NVT.R.....SB32
QNGVKAT--V..D.MS..KLSKEN--DDM..Q.V..VS.VAARTEAN..R.T.Y.....B16B6
TAGDTNGKT.T--E.V.....N.L.Y..LTRKNS.....SAMQAGGNSQADAKTEQVEQSM..Q.E..DEKE...--TDQNJV.R..Y.....M982
TAGVNGGQVGTKT..QV.....N.L.Y..LLTREN.....NNSVMQAVKNSS..AD.K.KQIE.SMFLQGERT.ENKIPQEQQGIV.L.F.Y.....FA19
NKHTIEING.T--MVAV.....E.M..QLW--QQAEGGKPENNSL..Q.E..AT.KM..--G.NY..I.T.D--Q..EGKQQVKDNSL..Q.E..AT.KM..A--G.NY..V.T.D--AP205
N..TVEING.T--MVAV.....E.M..QLW--Q..EGKQQVKDNSL..Q.E..AT.KM..A--G.NY..V.T.D--AP37

YITDGKTSYSPSGDKKRDKNAVAENVDAEKKLTGELKHDGT--NPVFSIEANFNNSNAAFTGTATATN--FVLDGKNSQNKNTPINITTKVNGAFYCPKA.....EAGAN
S..E....A....E.S....N....T.....Q--..K.N.T.QSGK.D.....KD--LA.....T.GTSKVNFTA...--.....DL63
S..E....A....E.S....D.S..N.T.....N.-T..K.N.EL.G.-..D.....N..TS.AK.....PAK
LS..S.....EN..L.....N.VD.T.KGQ.I..NQ--T..T.D.T.KGGK.N.....N.--VA..PQSTQGTSNWNFTA...--.....N.....SB12
G.D....TT.....D.N..D.T..T.....N.-..T.N.S.QSGK.D.....N.--VA..PQ.T.TTSRVNFTA...--.....N.....SB29
G.D....TT.....L..D.N.TD.....A.NQ--T..R.N.D.K.ND..K.....E--..N..TG..Q..K.E.....N.....N.....SB30
G.D....AT..RQ....P....A..NN.....TS.....NQ--..N.K.T.Q.GR.D.E.....E.....D..G--.....D.....D.....SB32

FIG. 15 D.

..AN.-.W.GEASNQEGG.-R...D...ST..IS.T.TAK.RT-S.A.T.T.MIKD--.G.S.V.KTGENG.AL.PQ.TG.SHYTHI-EAT.S.G...:KN.
H.AN.-.W.GNASD.EGG.-R...T.N..D..I..K.TAENRQ-AQT.T..GMIQG--.G.E...KTAESG.DL.Q..TTRTPKAYITDA..K.G.....
R.AN.-.W.GKASNAT.G.-R.K.T.N.DR.EI..T.TAENRS-EAT.T.D.MIEG--.G.K...KTG.DG.AP.QN..TVTHKVHIANAE.Q.G...:N.
AQVSKENNWVATA.DD.KSGYRT..D..GN.N.S.K.LFDKN.V...TVD.KIDG--.G..K.KTSDEG.AL.SGS.RYE.VKF.DVA-.S.G...:T.
ALVSKG.NWIAEA.NN.ESGYRT..D.N.SD..VN.K.-FDKG.V...TVD.TI.G...TVD.TI.G...T.G.I.S.KTSDSG.AL.AGS..HG.AVFSDI-...G...:T.
AP37

SELGGYFTYGN-STATNSESSSTVSSSNNSKNARAAYVFGAR-QQVETT-K*

T	-NPTDKN.....EK.....KK.....-	*	DL63
	KNP.....P.PP..P..S.....KK-.....N.*		PAK
T	-PTDK.....P.....	*	SB12
T	-NPTDDN.....P.-.A.....KK-.....N.*		SB29
T	KNP.DK.....P.PP..P.....KK-.....KNN.*		SB30
	KDTITK.T.....P.PP..P.....KK-.....N.*		SB32
I.M.	S.SFP.	APEGKQE-----K.S.....KR..LVQ*		B16B6
E	..W.A.P.DKQ.EKAT-----AT..DGNSASS.T.....KR..PVQ*		M982	
E	..W.A.P..EQ.KNA-----E.GNGNSASS.T.....KR.KLVK*		FA19	
A	..Q.HHKSENGSVGA-----K-...KK*		AP205	
G	..Q.HHKSDMGSVGA-----K-R..I.K*		AP37	

FIG.16A'.

FIG.16A'.

FIG.16A''

FIG.16A".

FIG.16B'.

FIG.16B'.

K E T L I
 S A L D G V G N
 422
 T K K E L K H T V K R E T E T E T 460
 E F S K H V K Y R K D K E A V F
 E T S S V E T E K D K N A V A
 K K I S C A E T E K E K N A K E
 F D S C L K E K E K R D L K K E
 D N L N S C P L K E K E K R D L E G T
 T N V Y S D P K D K D K L E G T
 K K V Y E D K D K D H R K L G G Y F T
 F G M K S G T D H R S E G N Y
 K E P T D S E G N Y
 Q T A T T N T Y Y Q F L L G H R T P K A S G
 A T T N T Y Y Q F L L G H R T P K A S G
 S Y S T K G D T Y G F W S G
 G N P V F S I E A N F N S S N A F T A T N Q S N K N Q S N K N Q S N K N Q S
 660
 K coo-
 T
 T E V Q Q
 F V A R E V A
 645
 D G 586
 500

FIG.16B'.

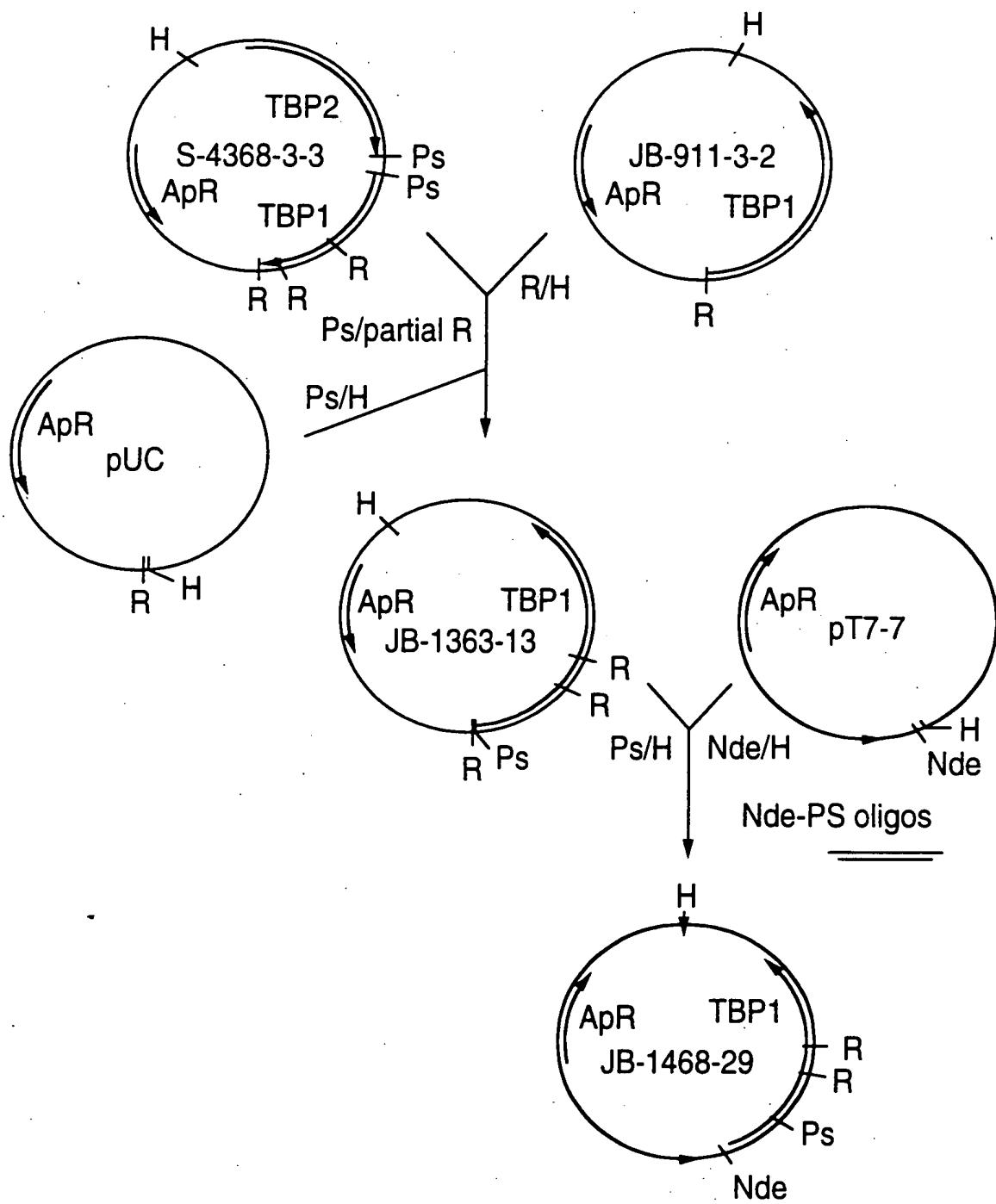


FIG.17.

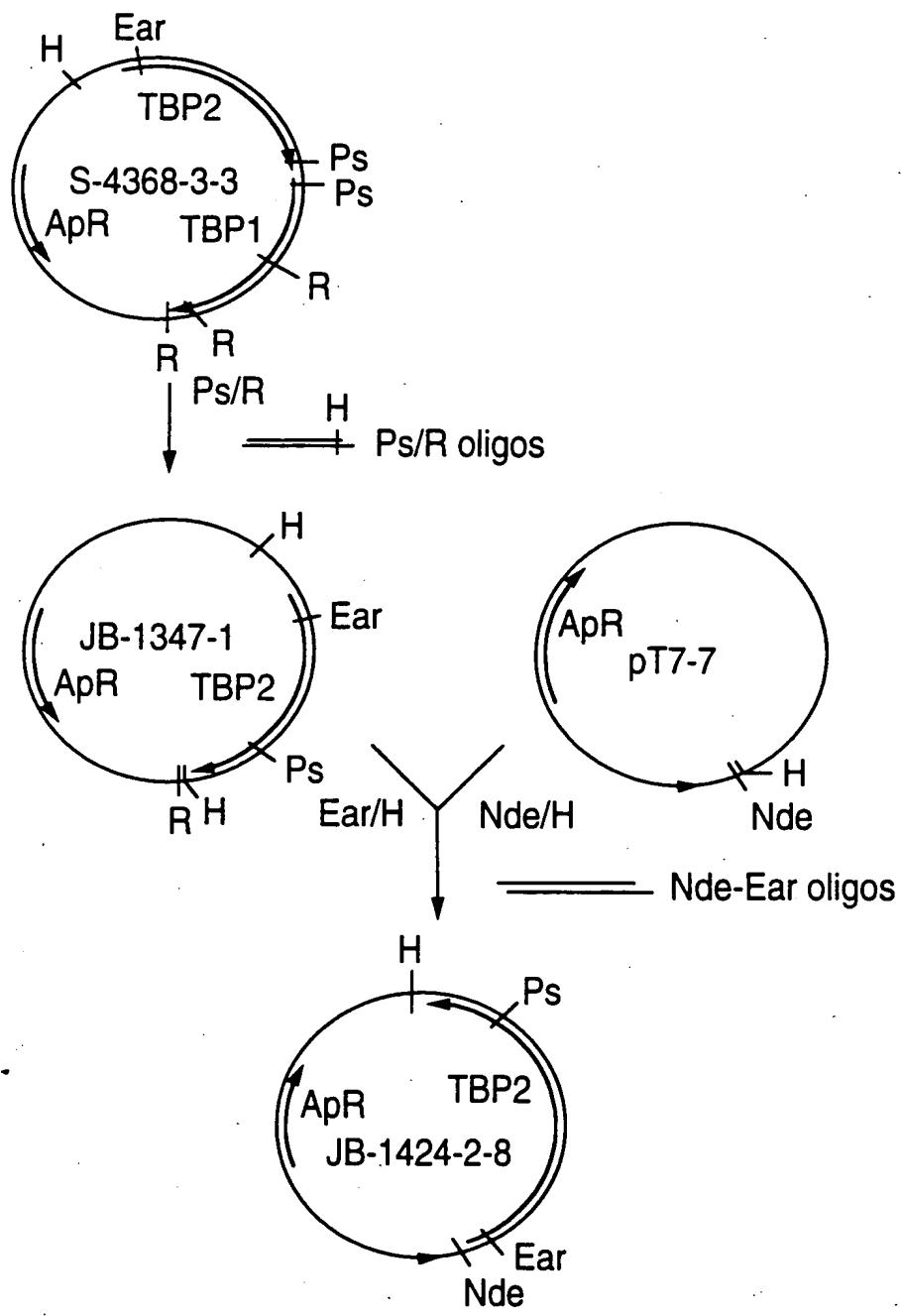


FIG.18

FIG.19. Oligonucleotides to expresss TBP2 with no signal sequence.

Ear I
Nde I
TATGTGTTCTGGTGGTTCTTCGACGTTGACAAACGTTCTAACACTCCCTCTTCT
ACACAAGAACCAACCAAGAAAGCTGGAAACTGTTGC

ATG start codon is underlined
TGT cysteinr of mature protein is double underlined

FIG. 20 A.

Sequence of oligonucleotide pairs (A, B, C and D) for constructing TBP1 and TBP2 expression plasmids

Oligonucleotide pair A (Seq. ID 86 and 87) to join the T7 promoter and Eagan TBP1 gene

Nde I

TATGGAAACTCAAAGTATAAAAGATAACAAAAGAAGCTATATCATCTGAAGT...
ACCTTTGAGTTCATATTTCATATGTTCTATGTTCTCGATATAGTAGACTTCA...

Pst I

...GGACACTCAAAGTACAGAAGATTCAGAATTAGAAACTATCTCAGTCACTGCA
...CCTGTGAGTTCATGTTCTAAGTCTTAAGTCTAAATCTTGTATAGACTCAGTG

Oligonucleotide pair B (Seq. ID 88 and 89) to join the T7 promoter and Eagan TBP2 genes through the *E. coli* 1pp leader

Nde I

TATGAAAGCTACTAAACTGGTTCTGGGTGCTGTTATCCTGGTTCCACTCTG...
ACTTTCGATCATTGACCAAGACCCACGACAATAGGACCAAGGTGAGAC...

Ear I

...CTGGCTGGTTTGTAGCGGGAGGTGGTTGATGTAGATAACGTCTCTAATACCCCGCTCTCT
...GACCCACCAACATGCCCTCCACCAACAAACTACATCTATTGCAGAGATTATGGGGGAGAAGATT

FIG. 20B.

Oligonucleotide pair C (Seq. ID 90 and 91) to join the T7 promoter and Eagan TBP2 genes throught the *E. coli* rlp B leader

Nde I

TATGCCGATATCTGGCAACACATTGTTGTTATCTGGCGGTGTTAATCACCGGCTG...
ACGCTATAGACCGGTGTAACAAACAATAGAGACCGGCCACAATTAGTGGCGAC...

Ear I

...GTTGTAGCGGGAGGTGGTTCTTTGATGTAGATAACGTCTCTAATACCCCTCTTCT
...CAACATCGCCTCCACCAAGAAAACATACATCTATTGCAGAGATTATGGGGAGAAGATT

Oligonucleotide pair D (Seq. ID 92 and 93) to join the T7 promoter and Eagan TBP2 genes throught the *E. coli* pal leader

Nde I

TATGCCAACTGAAACAAAGTGGCTGAAAGGGCTGATGATTGCTCTGCCCTGTATTGGCAA...
ACGTTGACTTGTGTTACCGACCTTCCCGACTACTAACGAGACGGACAATACCGTT...

Ear I

...TTGCTGGTTGTAGCGGGAGGTGGTTCTGTAGATAACGTCTCTAATACCCCTCTTCT
... AACGACCAACATCGCCTCCACCAAGAAAACATCTATTGCAGAGATTATGGGGAGAAGATT

ATG start codons are underlined
TGT coding for Cys of lipoproteins are double underlined
TGT may be replaced by TCC coding for Ser to secrete non-lipoprotein

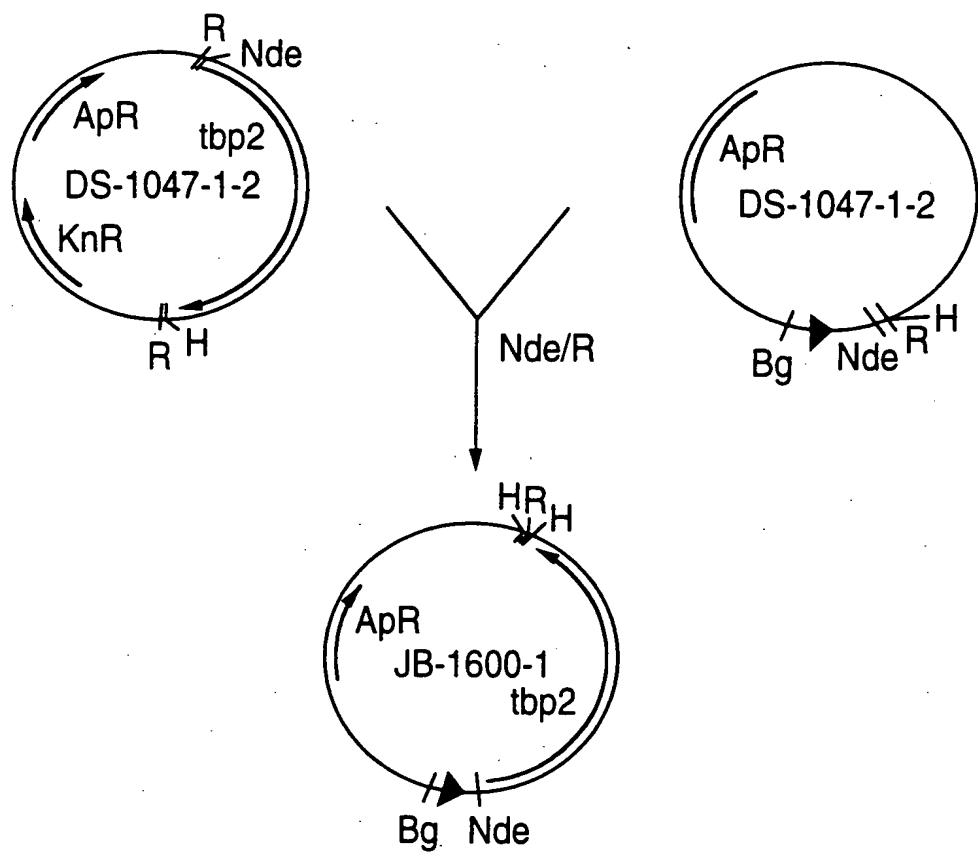


FIG.21.

1 2 3 4 5 6 7

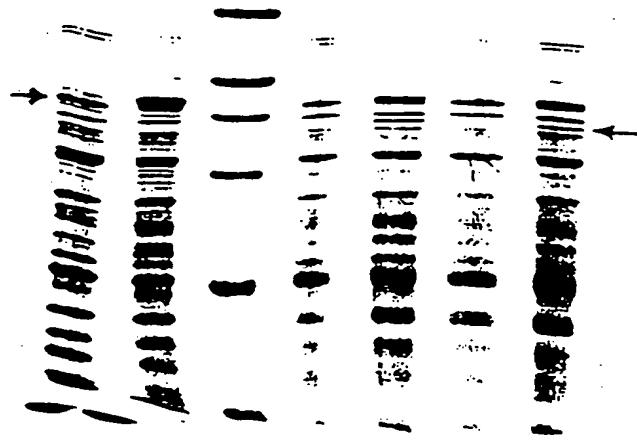


FIG.22.

PURIFICATION OF rTBP1/ rTBP2 FROM *E. COLI*

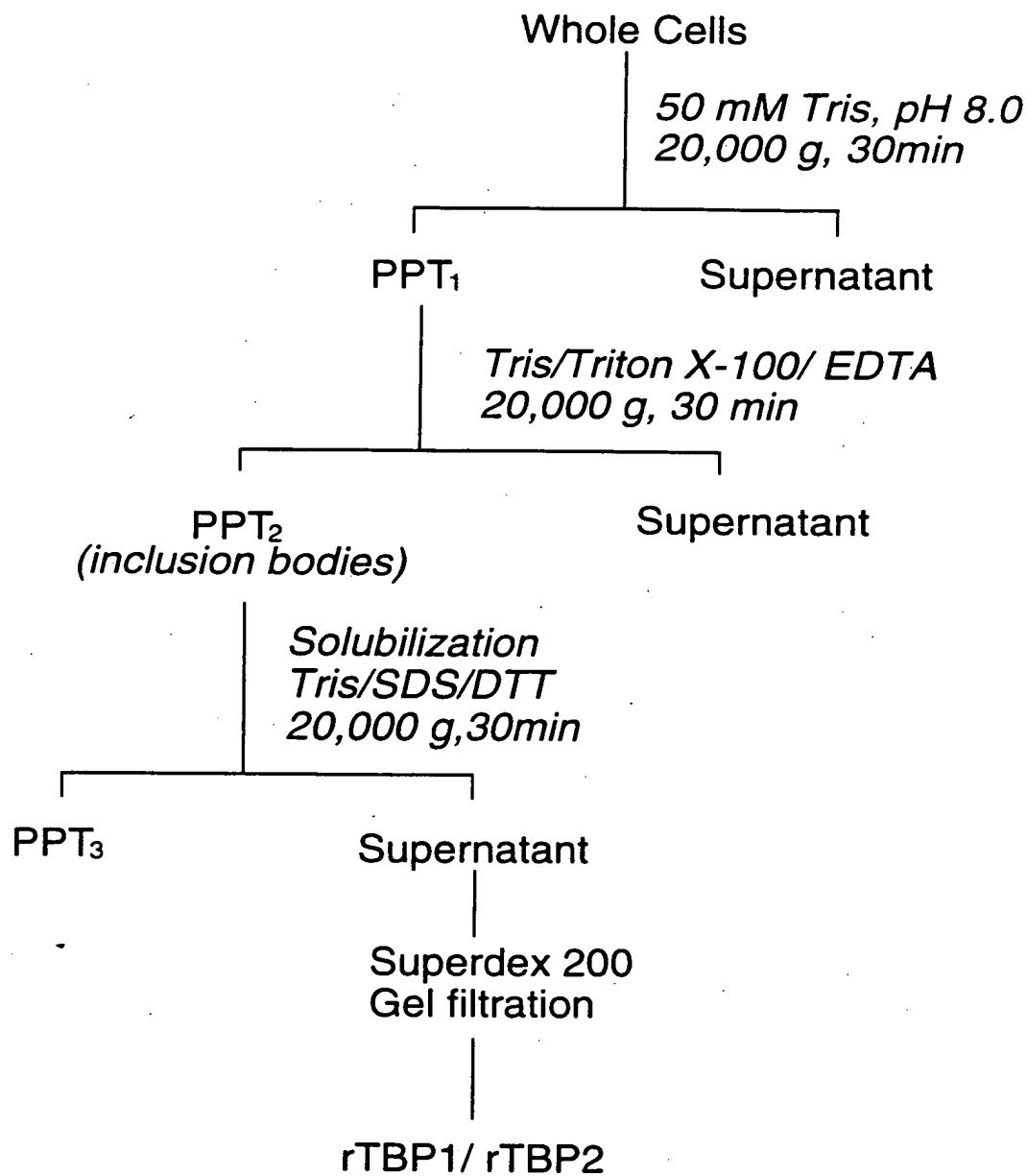
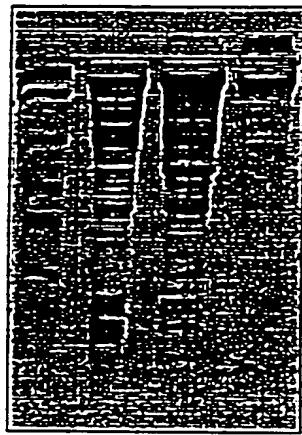


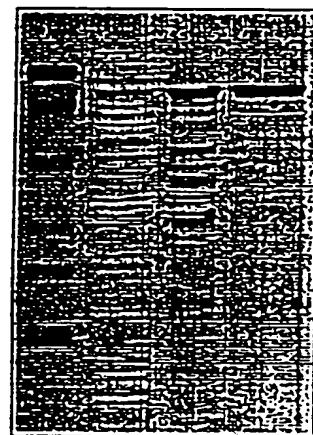
FIG.23.

rTBP1



1 2 3 4

rTBP2



1 2 3 4

FIG 24

Kinetics of Antibody Response to TBP1/TBP2 in Mice

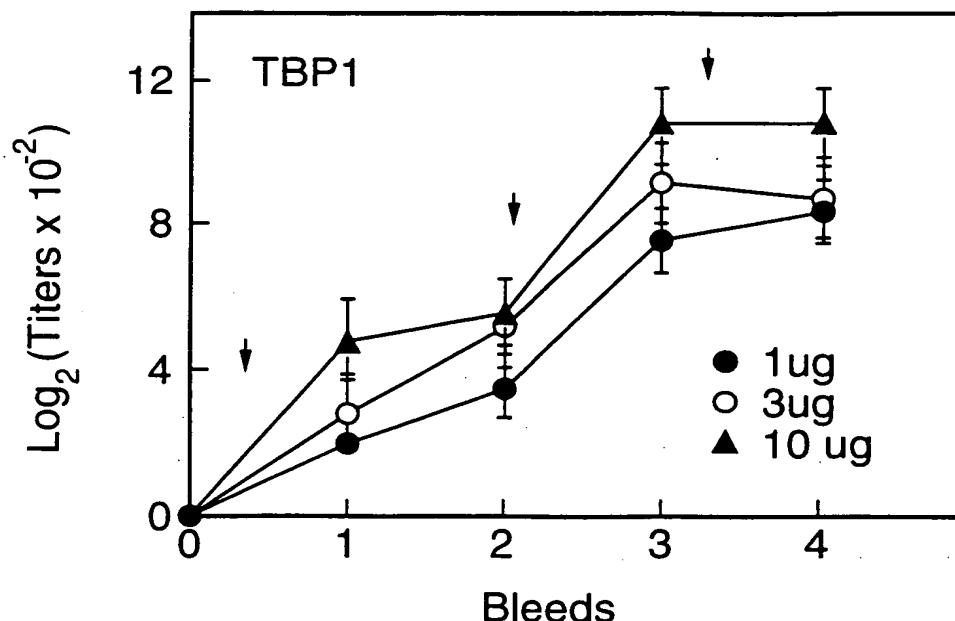


FIG.25A.

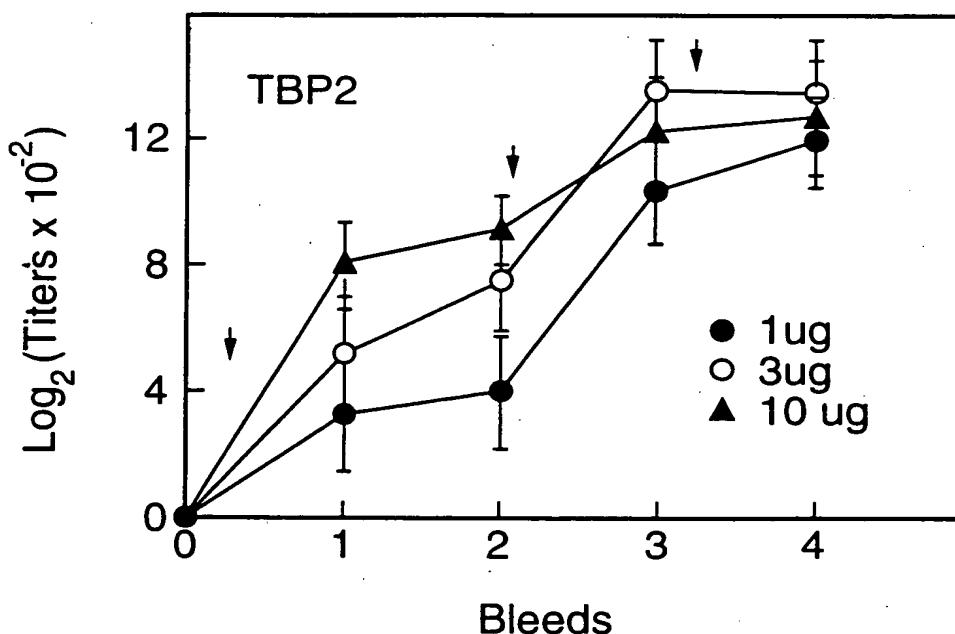


FIG.25B.

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15

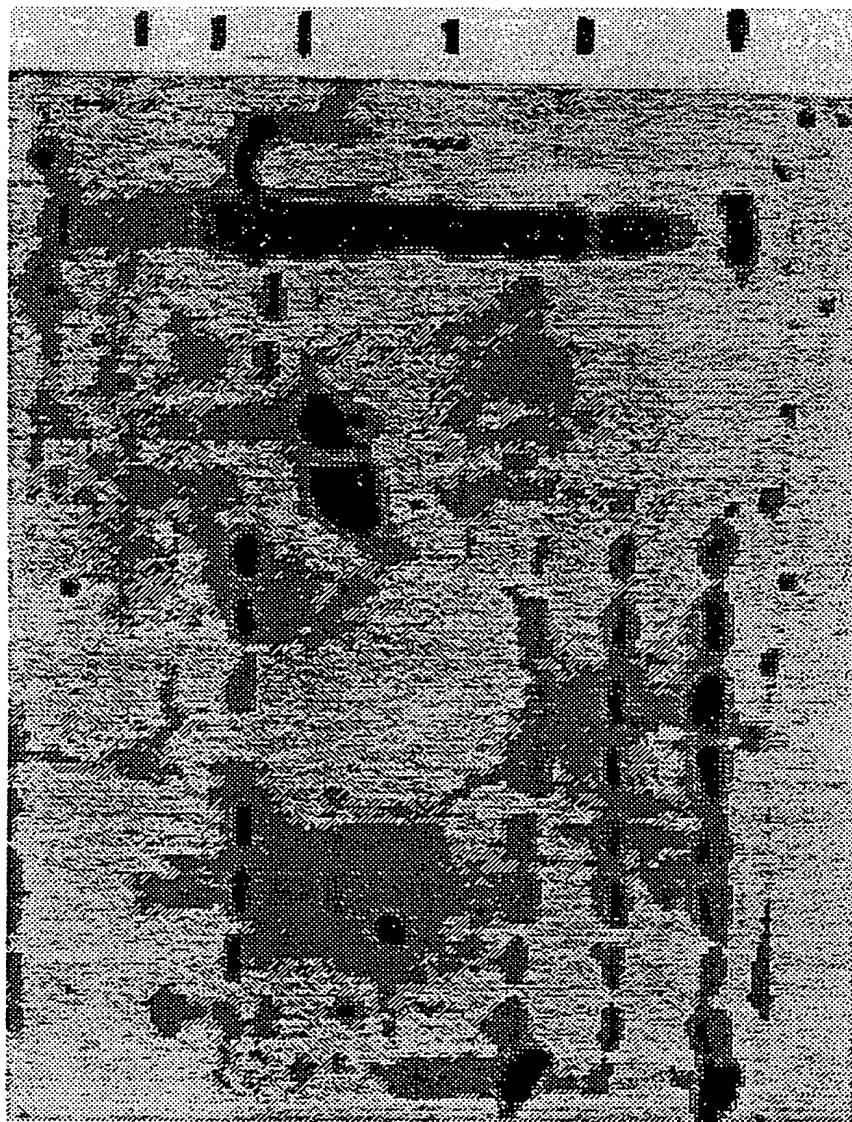


FIG.26.

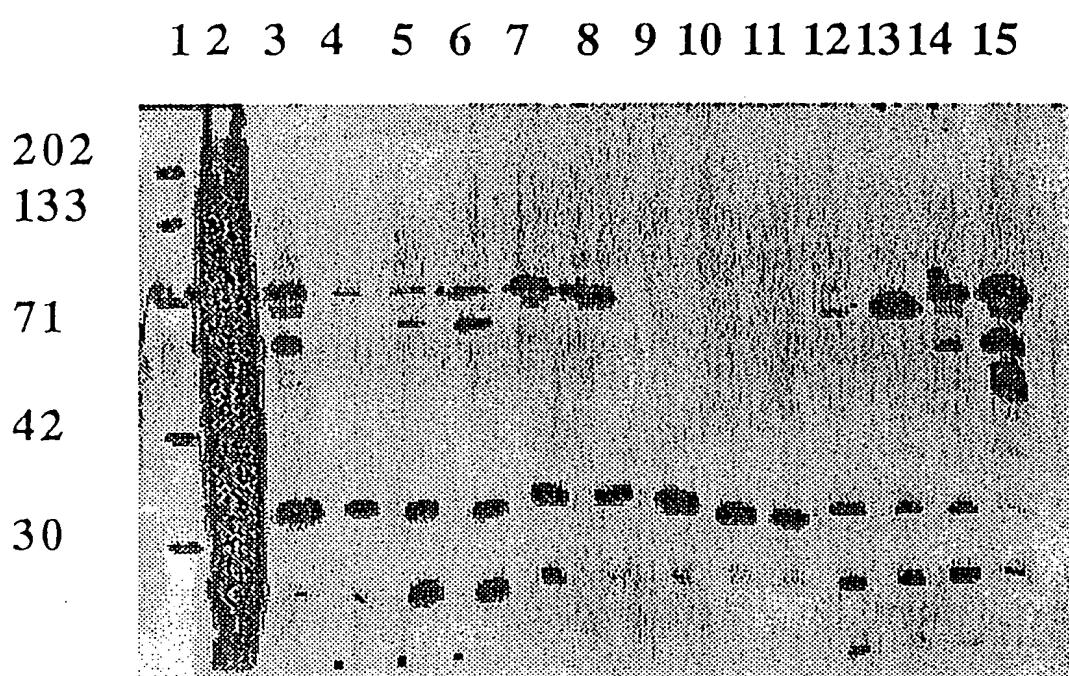


FIG. 27.

Construction of plasmids pUHIT1KFH and pUHIT1KFP

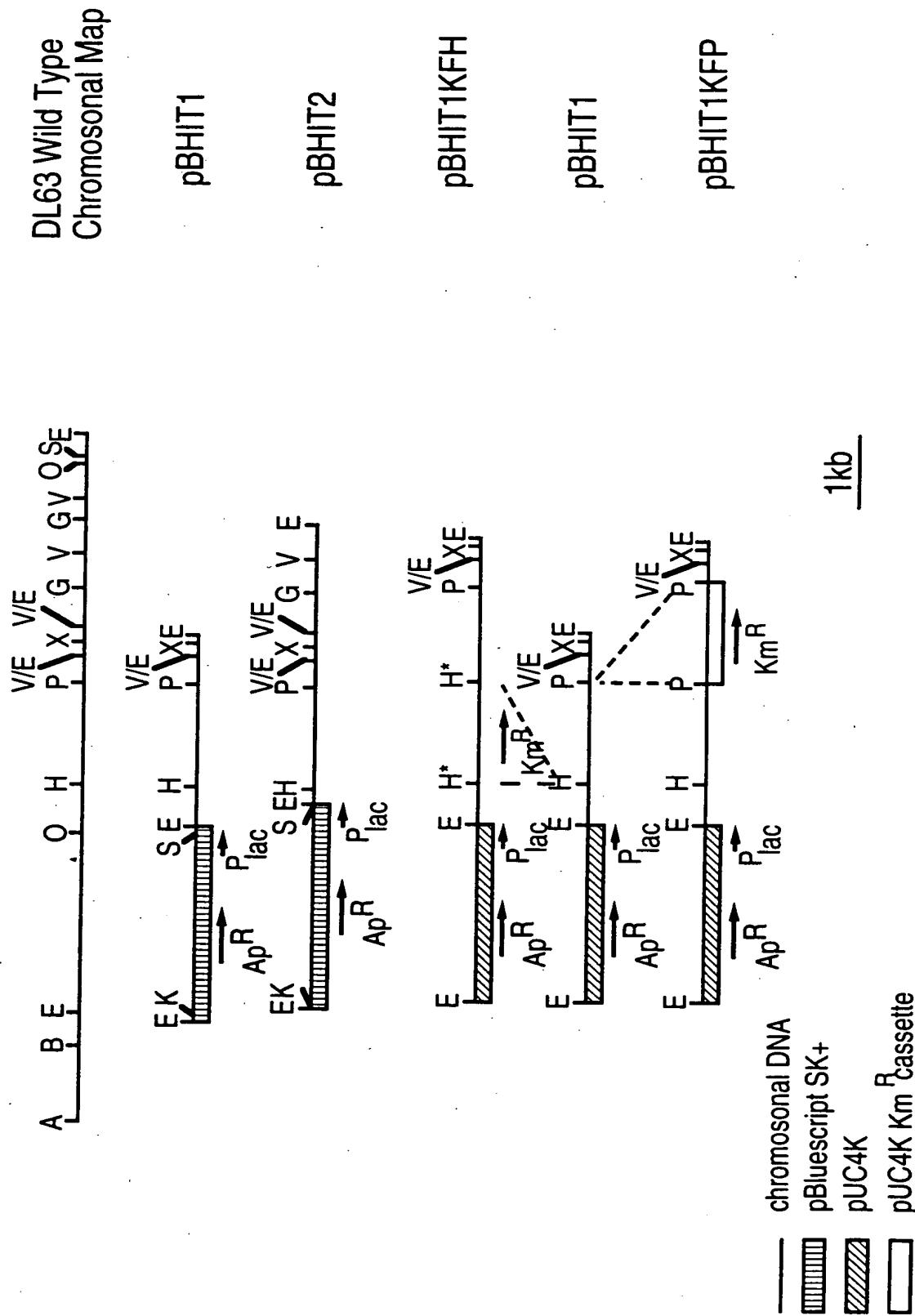
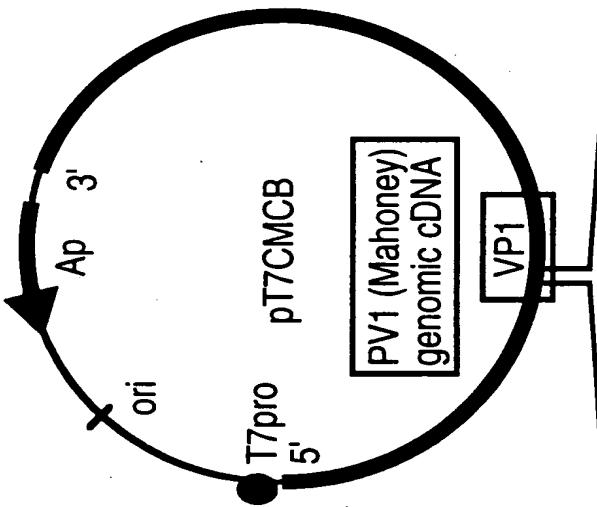


FIG. 28.



Sal I

nt 2753 G TC GAC AAC CCA GCT TCC ACC ACC AAT AAG GAC A AG CTT 2791
 CAG CT G T^TG GGT CGA AGG TGG TGG TTA TTC CTG TTC GA A
 aa1094 V D **N P A S T T N K D** K L 1102

Clone Sequence encoded

SEQ. Viable virus
 ID NO: recoverd/ strain
 designation

Hind III

nt 2753 G TC GAC AAC CCA GCT TCC ACC ACC AAT AAG GAC A AG CTT 2791
 CAG CT G T^TG GGT CGA AGG TGG TGG TTA TTC CTG TTC GA A
 aa1094 V D **N P A S T T N K D** K L 1102

Clone Sequence encoded

SEQ. Viable virus
 ID NO: recoverd/ strain
 designation

pT7XLD	NPASTTNKD	132	Yes / PV1-XLD
pT7TBP2A	NPASTTSLEGGFYGPKD	133	Yes / PV1TBP2A
pT7TBP2B	NPASTTSLEGGFYGKD	134	Yes / PV1TBP2B
pT7TBP2C	NPASTTLEGGFYGPKD	135	Yes / PV1TBP2C
pT7TBP2D	NPASTTLEGGFYGKD	136	Yes / PV1TBP2B

FIG. 29.

FIG. 30.

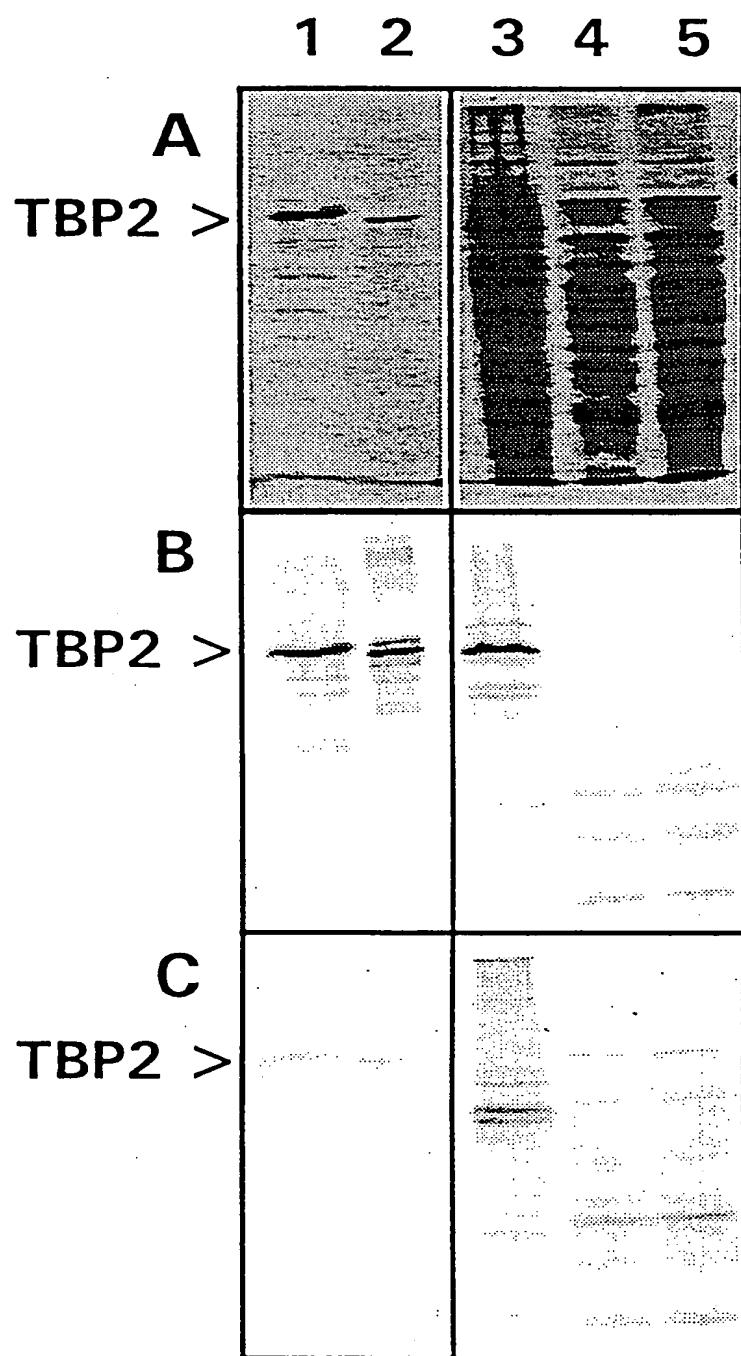


FIG.31A

Eagan Tbp2

MKSVPPLISGGGLSFLLSACSGGGSFDVNVSNTPSSKPRYQDDTSNQRKKS
Signal Sequence
DS-1466-1-18

↓
NLKKLFIPLGGGMKLVAQNLRGDNKEPSFLNEDDYISYFSSLSTIEKDVK
DS-1466-4-3

↓
DNNKNGADLIGSIDEPSTTNPPEKHHGQKYVYSGLYYTPSWSLNDSKNK
DS-1466-4-3

YLGYYGYAFYYGNKTATNLPVNGVAKYKGTWDFITATKNGKRYPLLSNGS

HAYYRRSAIPEDIDLENDSKNGDIGLISEFSADEFGTKKLTGQLSYTKRKT
DS-1466-5-1

↓
NNQPYEKKKLYDIDIYSNRFRGTVKPTEKDSEEHPFTSEGTLEGGFYVG
DS-1466-4-1

↓
PNAEELGGKFLATDNRVFGVFSAKETEETKKEALSKETLIDGKLITFSTK

FIG.31B

DS-1457-3-1

KTDAKTNATTSTAANTTTDTTANTTITDEKNFKTEDDISSFGEADYLLIDKY
DS-1466-1-4 DS-1466-7-9 DS-1466-3-1 DS-1466-3-4
↓ ↙ ↓
PIPLL PDKNTNDFISSKKHHTVGNKRYKVEACCSNLSYVKFGMYYEDPLKE
DS-1466-2-6

KETETETEKEKEKEKDKEKEKQTAATTINTYYQFLIGHRTPKDDIPK
DS-1461-1-1 DS-1466-1-14
↓ ↙ ↓
TGSAKYHGSWFGYITDGKTSYSPSGDKKRDKNAVAEFFNVDFAEKKLGTGEI

KRHDTGNPVFSIEANFNNSSNAFTTGTATATNFVIDGKNSQNKNTPINITT
DS-1461-8-1
↓
KVNGAFYGPKASELGGYFTYNGNSTATNSESSTVSSSSNSKNARA AVVF
GARQQVETTK*

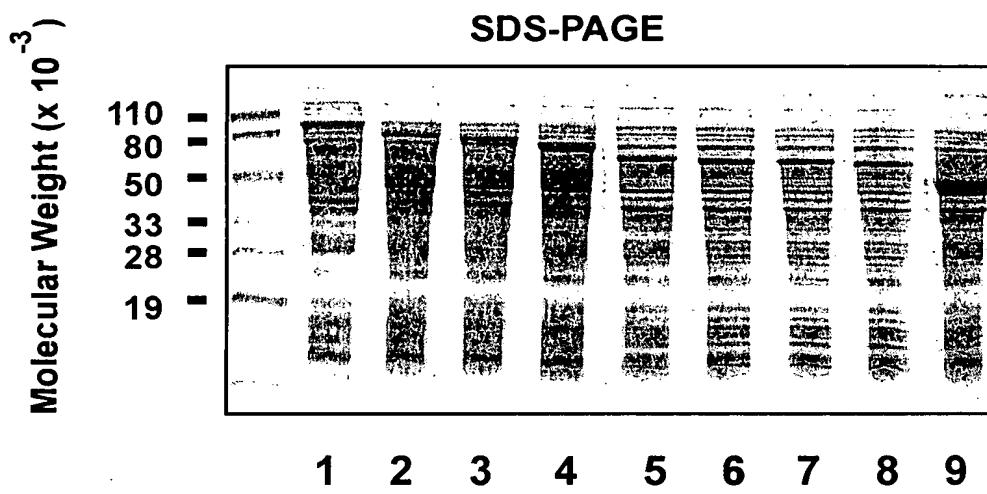


FIG 32 A.

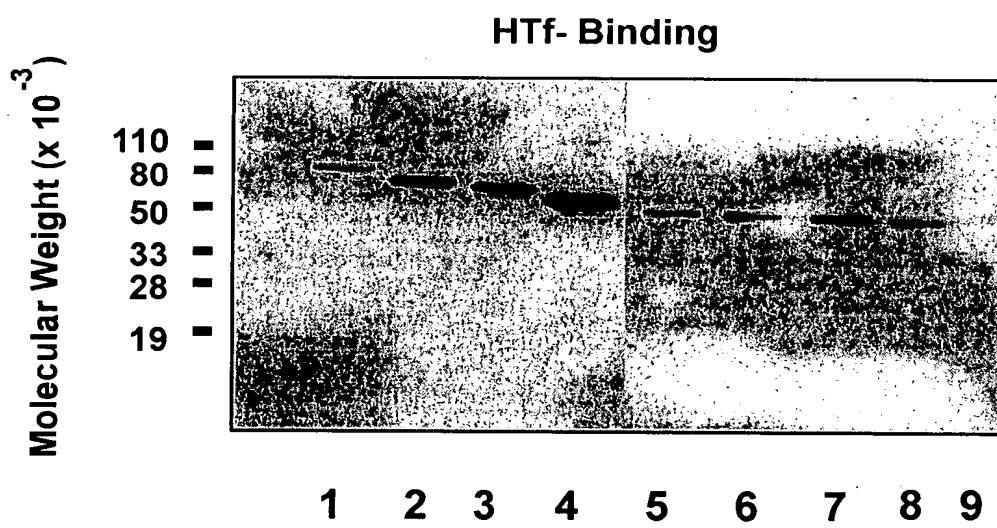


FIG 32 B.